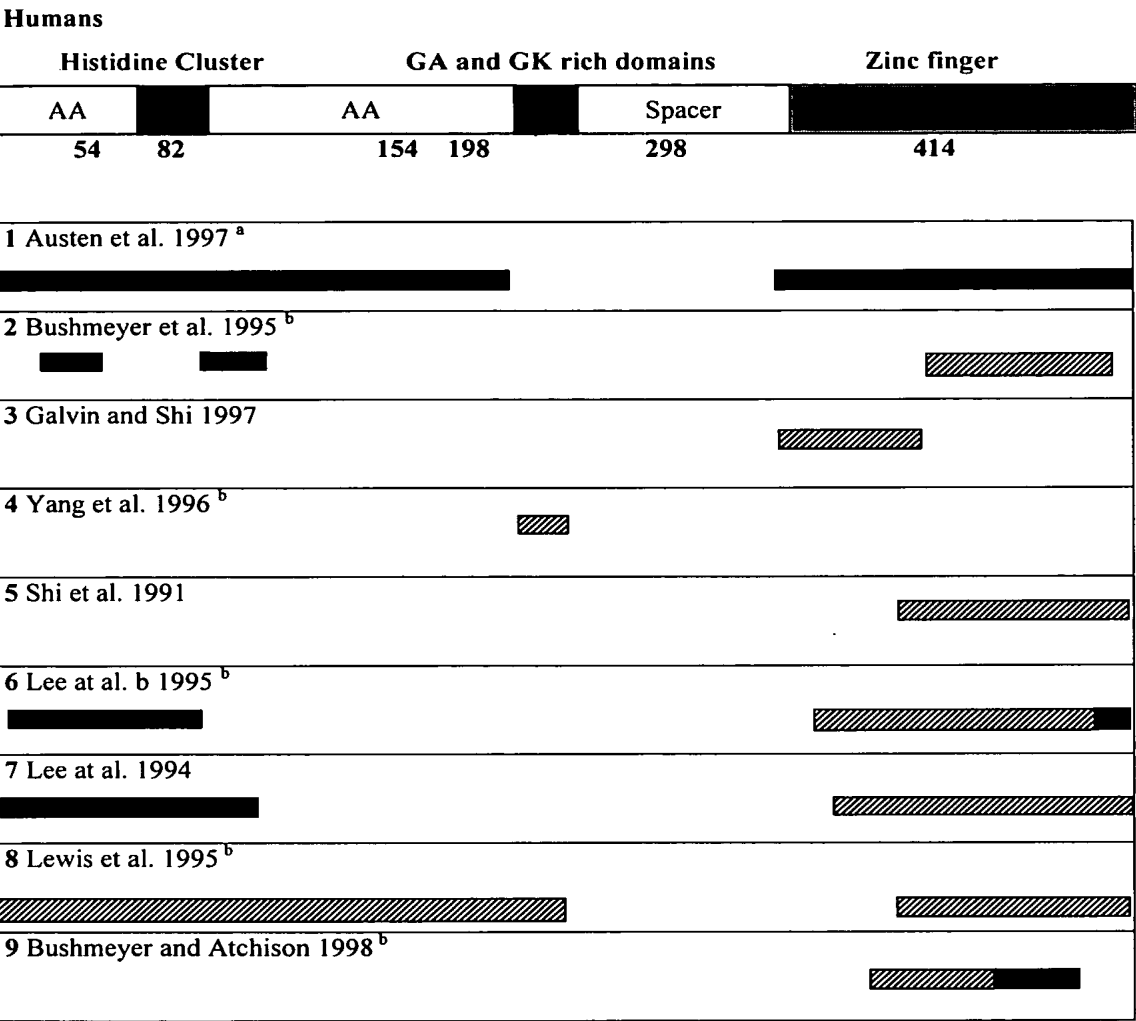


Figure 1



a Activation and DNA-binding domains overlapping

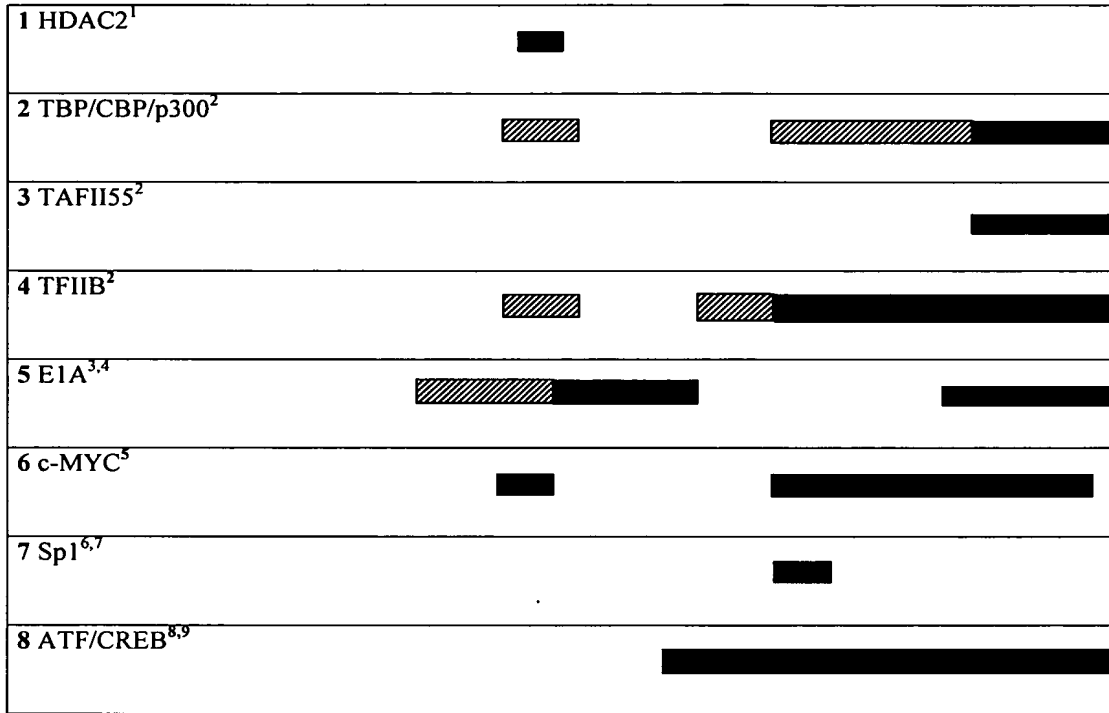
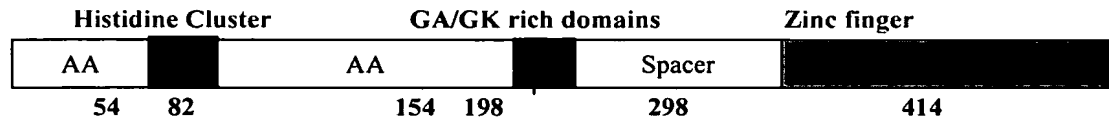
b Gal⁴ DNA-binding domain fusion

Activation

Repression

Figure 2

Humans





 Strong interaction
 Weak interaction

Figure 3

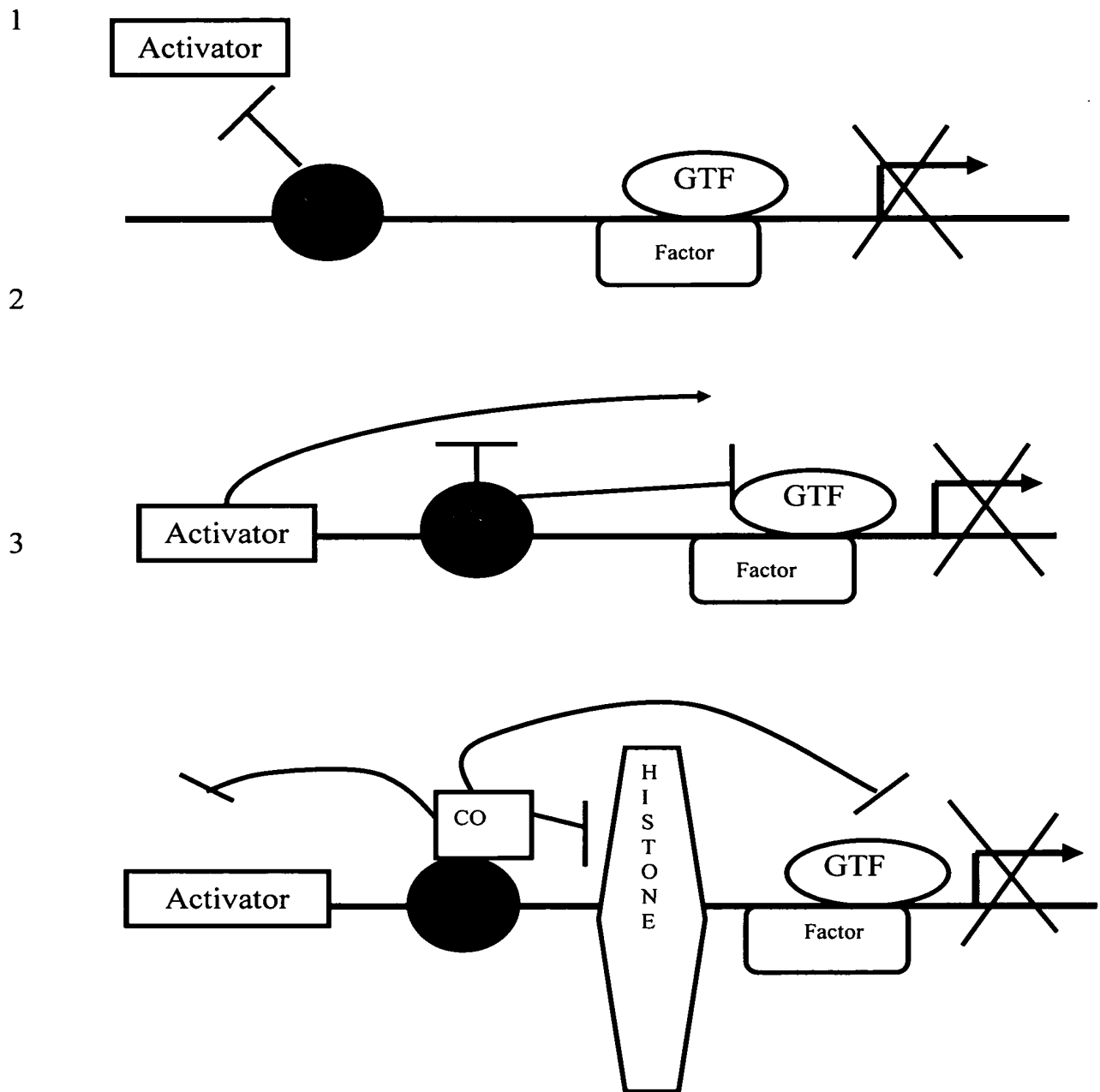
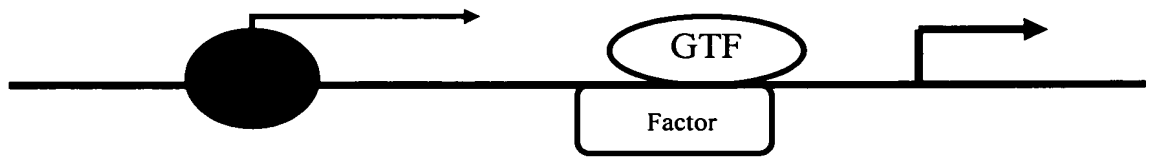
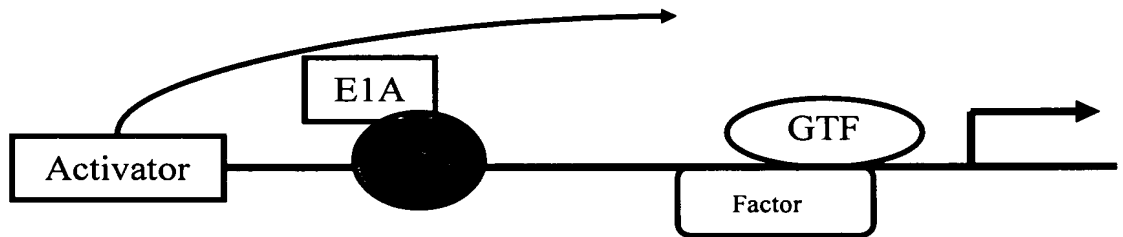


Figure 4

1



2



3

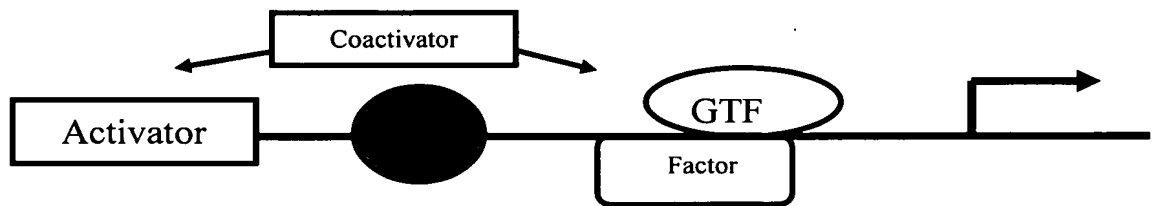
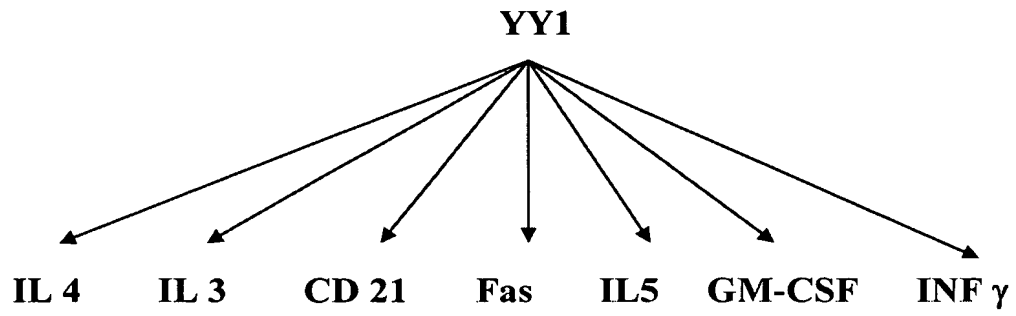


Figure 5



Activation and inhibition by YY1

Figure 6

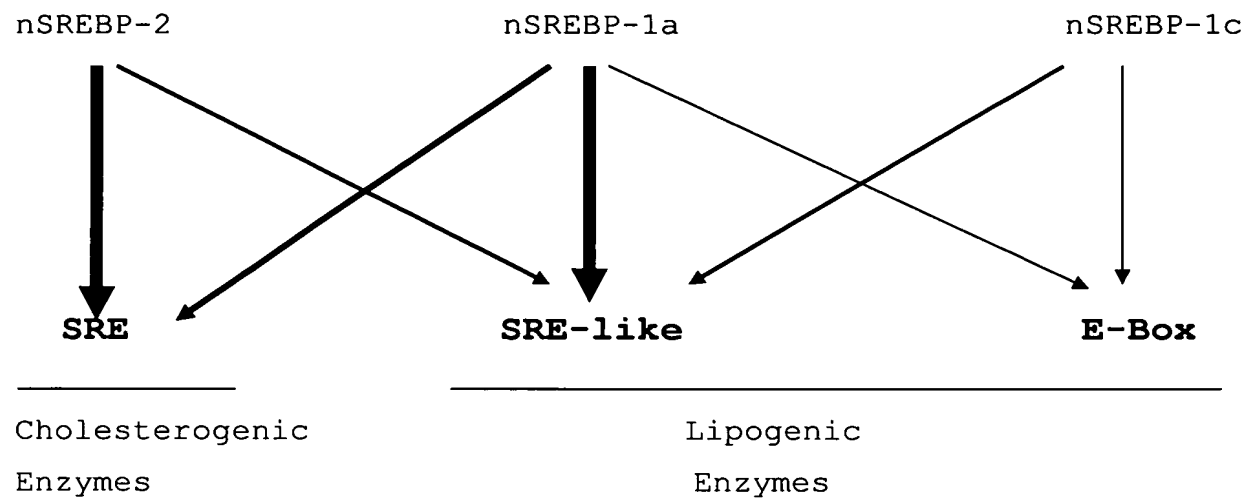
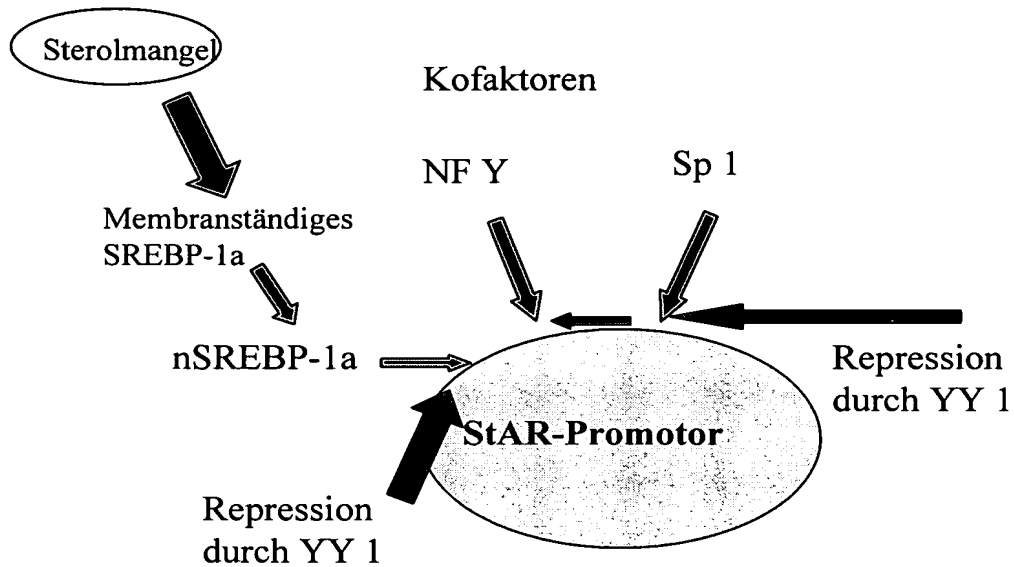


Figure 7



Key:

Sterolmangel = Sterol deficiency

Kofaktoren = Cofactors

Membranständiges SREBP-1a = Membrane bound SREBP-1a

Repression durch YY1 = Repression by YY1

Figure 8

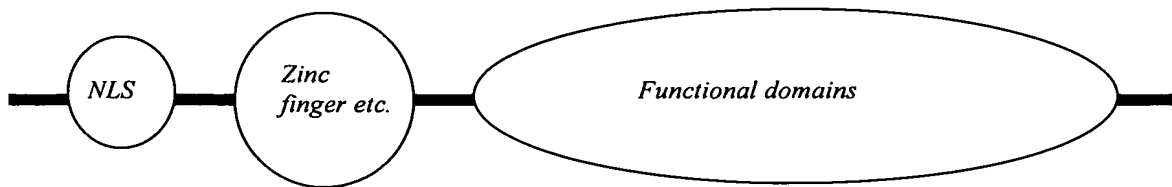


Figure 9 - 1. Continued

GGC GAC GAC TCG GAC GGG CTG CGC GCC GAG GAC GGG TTC GAG GAC CAG ATC CTC ATT CCG
GGC GAC GAC TCG GAC GGG CTG CGC GCC GAG GAC GGG TTC GAG GAC CAG ATC CTC ATT CCG GG
GAC GAC TCG GAC GGG CTG CGC GCC GAG GAC GGC TTC GAG GAC GAG ATC CTC ATC CCG

G D D S D G L R A E D G F E D Q I L I P G
D D S D G L R A E D G F E D Q I L I P
G D D S D G L R A E D G F E D Q I L I P

GTA CCC GCG CCG GCC GGC GGA GAC GAC GAC TAC ATC GAG CAG ACG CTG GTC ACC GTG GCG
GTA CCC GCG CCG GCC GGC GGA GAC GAC GAC TAC ATC GAG CAG ACG CTG GTC ACC GTG GCG
GTG CCC GCG CCG GCC GGC GGC GAC GAC GAC TAC ATC GAG CAG ACG CTG GTC ACC GTG GCG

V P A P A G G D D D Y I E Q T L V T V A
V P A P A G G D D D Y I E Q T L V T V A
V P A P A G G D D D Y I E Q T L V T V A

GCG GCC GGC AAG AGC GGT GGC GGG TCT TCG TCG GGC GGC GGC CGC GTT AAG AAG GGC GGC
GCG GCC GGC AAG AGC GGT GGC GGG TCT TCG TCG GGC GGC GGC CGC GTT AAG AAG GGC GGC
GCG GCC GGC AAG AGC GGC GGC GGC TCG TCG GGC GGC GGC CGC GTT AAG AAG GGC GGC

A A G K S G G G S S G G G R V K K G G
A A G K S G G G S S G G G R V K K G G
A A G K S G G G S S G G G R V K K G G

GGC AAG AAG AGC GGC AAG AAG AGT TAC CTG GGC AGC GGG GCC GGC GCG GCG GGC GGT GGC
GGC AAG AAG AGT GGC AAG AAG AGT TAC CTG GGC AGC GGG GCC GGC GCG GCG GGC GGT GGC
GGC AAG AAG AGC GGC AAG AAG AGT TAC CTG GGC GGC GGG GCC GGC GCG GCG GGC GGC

G K K S G K K S Y L G S G A G A A G G G
K K S G K K S Y L G S G A G A A G G G
G K K S G K K S Y L G G G A G A A G G G

GGC GCC GAC CCG GGT AAT AAG AAG TGG GAA CAG AAG CAG GTG CAG ATC AAG ACC CTG GAG
GGC GCC GAC CCG GGT AAT AAG AAG TGG GAA CAG AAG CAG GTG CAG ATC AAG ACC CTG GAG
GGC GCC GAC CCG GGT AAT AAG AAG TGG GAA CAG AAG CAG GTG CAG ATC AAG ACC CTG GAG

G A D P G N K K W E Q K Q V Q I K T L E
G A D P G N K K W E Q K Q V Q I K T L E
G A D P G N K K W E Q K Q V Q I K T L E

GGC GAG TTC TCG GTC ACC ATG TGG TCT TCA GAT GAA AAA AAA GAT ATT GAC CAT GAA ACA
GGC GAG TTC TCG GTC ACC ATG TGG TCT TCA GAT GAA AAA AAA GAT ATT GAC CAT GAA ACA
GGC GAG TCG TCG GTC ACC ATG TGG TCT TCG GAT GAA AAA AAA GAT ATT GAC CAT GAA ACA

G E S V T M W S S D E K K D I D H E T
G E S V T M W S S D E K K D I D H E T
G E S V T M W S S D E K K D I D H E T

GTG GTT GAA GAG CAG ATC ATT GGG GAG AAC TCA CCT CCT GAT TAT TCT GAA TAT ATG ACA
GTG GTT GAA GAG CAG ATC ATT GGG GAG AAC TCA CCT CCT GAT TAT TCT GAA TAT ATG ACA
GTG GTT GAA GAG CAG ATC ATT GGA GAG AAC TCA CCT CCT GAT TAT TCT GAA TAT ATG ACA
V V E E Q I I G E N S P P D Y S E Y M T V
V E E Q I I G E N S P P D Y S E Y M T
E E Q I I G E N S P P D Y S E Y M T

Figure 9 - 2. Continued

```

GGC AAG AAA CTC CCT CCT GGA GGG ATA CCT GGC ATT GAC CTC TCA GAC CCC AAG CAA CTG
GGC AAG AAA CTC CCT CCT GGA GGG ATA CCT GGC ATT GAC CTC TCA GAC CCC AAG CAA CTG
GGC AAG AAA CTC CCT CCT GGA GGG ATA CCT GGC ATT GAC CTC TCA GAC CCC AAG CAA CTG

  G  K  K  L  P  P  G  G  I  P  G  I  D  L  S  D  P  K  Q  L
  G  K  K  L  P  P  G  G  I  P  G  I  D  L  S  D  P  K  Q  L
  G  K  K  L  P  P  G  G  I  P  G  I  D  L  S  D  P  K  Q  L

GCA GAA TTT GCC AGA ATG AAG CCA AGA AAA ATT AAA GAA GAT GAT GCT CCA AGA ACA ATA
GCA GAA TTT GCC AGA ATG AAG CCA AGA AAA ATT AAA GAA GAT GAT GCT CCA AGA ACA ATA
GCA GAA TTT GCC AGA ATG AAG CCA AGA AAA ATT AAA GAA GAT GAT GCT CCA AGA ACA ATA

  A  E  F  A  R  M  K  P  R  K  I  K  E  D  D  A  P  R  T  I
  A  E  F  A  R  M  K  P  R  K  I  K  E  D  D  A  P  R  T  I
  A  E  F  A  R  M  K  P  R  K  I  K  E  D  D  A  P  R  T  I

GCT TGC CCT CAT AAA GGC TGC ACA AAG ATG TTC AGG GAT AAC TCT GCT ATG AGA AAG CAT
GCT TGC CCT CAT AAA GGC TGC ACA AAG AGG TTC AGG GAT AAC TCT GCT ATG AAA AAG CAT
GCT TGC CCT CAT AAA GGC TGC ACA AAG ATG TTC AGG GAT AAC TCT GCT ATG AGA AAG CAT
* Zinkfinger
  A  C  P  H  K  G  C  T  K  M  F  R  D  N  S  A  M  R  K  H
  A  C  P  H  K  G  C  T  K  R  F  R  D  N  S  A  M  K  K  H
  A  C  P  H  K  G  C  T  K  M  F  R  D  N  S  A  M  R  K  H

CTG CAC ACC CAC GGT CCC AGA GTC CAC GTC TGT GCA GAA TGT GGC AAA GCG TTC GTT GAG
CTG CAC ACC CAC GGT CCC AGA GTC CAC GTC TGT GCA GAA TGT GGC AAA GCG TTC GTT GAG
CTG CAC ACC CAC GGT CCC AGA GTC CAC GTC TGT GCA GAA TGT GGC AAA GCG TTC GTT GAG

  L  H  T  H  G  P  R  V  H  V  C  A  E  C  G  K  A  F  V  E
  L  H  T  H  G  P  R  V  H  V  C  A  E  C  G  K  A  F  V  E
  L  H  T  H  G  P  R  V  H  V  C  A  E  C  G  K  A  F  V  E

AGC TCA AAG CTA AAA CGA CAC CAG CTG GTT CAT ACT GGA GAA AAG CCC TTT CAG-GTAGAGC
AGC TCA AAG CTA AAA CGA CAC CAG CTG GTT CAT ACT GGA GAA AAG CCC TTT CAG-GTAGAGC
AGC TCA AAG CTA AAA CGA CAC CAG CTG GTT CAT ACT GGA GAA AAG CCC TTT CAG-----

  S  S  K  L  K  R  H  Q  L  V  H  T  G  E  K  P  F  Q
  S  S  K  L  K  R  H  Q  L  V  H  T  G  E  K  P  F  Q
  S  S  K  L  K  R  H  Q  L  V  H  T  G  E  K  P  F  Q

CAGTTCCTGTTCCCCAAACTGCAAGCTAGGGTGCTGGTCAGGGTGGTTGATATCAAGCACTATGGGGCACC GGT
CAGTTCCTGTTCCCCAAACTGCAAGCTAGGGTGCTGGTCAGGGTGGTTGATATCAAGCACTATGGGGCACC GGT
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TGGGGTATTTTATTTCCCATCCCTCCTGTCTGCTTGGGTTCTGGTTACTGCTCGGGACTGCAGGTGTTACAGAT
TGGGGTATTTTATTTCCCATCCCTCCTGTCTGCTTGGGTTCTGGTTACTGCTCGGGACTGCAGGTGTTACAGAT
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GGGGGTGGAGGGATTATGCGAAGCACCCCCACACTAAATTTCTAGCAGGTTTACAAAACTCAACAGTTTTGTTT
GGGGGTGGAGGGATTATGCGAAGCACCCCCACACTAAATTTCTAGCAGGTTTACAAAACTCAACAGTTTTGTTT
-----

TG TAGT GAG TAGT GTT GAATT ACT GAT AGAGT GCTTATAAGT GCT GTTGGCTACAGCTCCAGGTGACACTTG
TG TAGT GAG TAGT GTT GAATT ACT GAT AGAGT GCTTATAAGT GCT GTTGGCTACAGCTCCAGGTGACACTTG
-----

```

Figure 9 - 3. Continued

GTGCTGCTTATAGAAGAC¹CGTGAGTTGACAGTTGGCATCACTAAATATCTTAATCATCTGTAGTCTACTTCCT
 GTGCTGCTTATAGAAGAC²CGTGAGTTGACAGTTGGCATCACTAAATATCTTAATCATCTGTAGTCTACTTCCT

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 AGAGTGTCTCTGAAAACACTCAAGCTGTAAATTTGCACTCAGCACAGCCCTTCTGTTTCTCAAGAACTAGCCAT

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 GGGTTGTTAGTATCAGAGATCCCAGTGTGTCTAGTTCTAAAATACCCTCA⁴AAGGGTTCCAGACGAGGAAGGAGG

⁵CaTGCTCAGCAGAATAGTAGGTGGTTTCCATCTAAGCAGTGAGCCATCGATCCCCAGGTTCTGGTCTCATTTGC
⁶CTTGCTCAGCAGAATAGTAGGTGGTTTCCATCTAAGCAGTGAGCCATCGATCCCCAGGTTCTGGTCTCATTTGC

CAAGAGGGTTGATATCTGGTTTTTTCCTTGACAG -TGC ACA
 CAAGAGGGTTGATATCTGGTTTTTTCCTTGACAG -TGC ACA
 ----- -TGC ACA
 C T
 C T
 C T

TTC	GAA	GGC	TGC	GGG	AAG	CGC	TTT	TCA	CTG	GAC	TTC	AAT	TTG	CGC	ACG	CAT	GTG	CGA	ATC
TTC	GAA	GGC	TGC	GGG	AAG	CGC	TTT	TCA	CTG	GAC	TTC	AAT	TTG	CGC	ACG	CAT	GTG	CGA	ATC
TTC	GAA	GGC	TGC	GGG	AAG	CGC	TTT	TCA	CTG	GAC	TTC	AAT	TTG	CGC	ACA	CAT	GTG	CGA	ATC
F	E	G	C	G	K	R	F	S	L	D	F	N	L	R	T	H	V	R	I
F	E	G	C	G	K	R	F	S	L	D	F	N	L	R	T	H	V	R	I
F	E	G	C	G	K	R	F	S	L	D	F	N	L	R	T	H	V	G	I
CAT	ACC	GGA	GAC	AGG	CCC	TAT	GTG	TGC	CCC	TTC	GAC	GGT	TGT	AAT	AAG	AAG	TTT	GCT	CAG
CAT	ACC	GGA	GAC	AGG	CCC	TAT	GTG	TGC	CCC	TTC	GAC	GGT	TGT	AAT	AAG	AAG	TTT	GCT	CAG
CAT	ACC	GGA	GAC	AGG	CCC	TAT	GTG	TGC	CCC	TTC	GAC	GGT	TGT	AAT	AAG	AAG	TTT	GCT	CAG
H	T	G	D	R	P	Y	V	C	P	F	D	G	C	N	K	K	F	A	Q
H	T	G	D	R	P	Y	V	C	P	F	D	G	C	N	K	K	F	A	Q
H	T	G	D	R	P	Y	V	C	P	F	D	G	C	N	K	K	F	A	Q

TCA	ACT	AAC	CTG	AAA	TCT	CAC	ATC	TTA	ACA	CAC	GCT	AAA	GCC	AAA	AAC	AAC	CAG	TGA
TCA	ACT	AAC	CTG	AAA	TCT	CAC	ATC	TTA	ACA	CAC	GCT	AAA	GCC	AAA	AAC	AAC	CAG	TGA
TCA	ACT	AAC	CTG	AAA	TCT	CAC	ATC	TTA	ACA	CAC	GCT	AAA	GCC	AAA	AAC	AAC	CAG	TGA
Zinc finger *																		
S	T	N	L	K	S	H	I	L	T	H	A	K	A	K	N	N	Q	*
S	T	N	L	K	S	H	I	L	T	H	A	K	A	K	N	N	Q	*
S	T	N	L	K	S	H	I	L	T	H	A	K	A	K	N	N	Q	*

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 AAAGAAGAGAGAAGACCTTCTCGACCCCGGGAAGCCTCTTCAGGAGTGTGATTGGGAATAAATATGCCTCTC
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 CTTTGTATATTATTTCTAGGAAGAATTTTAAAAATGAATCCTACACACTTAAGGGACATG
 CTTTGTATATTATTTCTAGGAAGAATTTTAAAAATGAATCCTACACACTTAAGGGACATG
 CTTTGTATATTATTTCTAGGAAGAATTTTAAAAATGAATCCTACACACTTAAGGGACATG

Figure 9 - 4. Continued

TTTGTATAAAGTAGTAAAAATTTAAAAAATACTTTAATAAGATGACATTGCTAAGATGC
TTTGTATAAAGTAGTAAAAATTTAAAAAATACTTTAATAAGATGACATTGCTAAGATGC
TTTGTATAAAGTAGTAAAAATTTAAAAA-TACTTTAATAAGATGACATTGCTAAGATGC

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TCTATCTTGCTCTGTAATCTCGTTTCAAAAACAAGGTGTTTTGTAAAGTGTGGTCCCAA
TCTATCTTGCTCTGTAATCTCGTTTCAAAAACAAGGTGTTTTGTAAAGTGTGGTCCCAA

CAGGAGGACAATTCATGAACCTTCGCATCAAAAGACAATTCTTTATACAACAGTGCTAAAA
CAGGAGGACAATTCATGAACCTTCGCATCAAAAGACAATTCTTTATACAACAGTGCTAAAA
CAGGAGGACAATTCATGAACCTTCGCATCAAAAGACAATTCTTTATACAACAGTGCTAAAA

ATG ATG ATG

Figure 10

Protein comparison

BBSHR

Homo sapiens

MASGDTLYIATDGSEMPAEIVELHEIEVETIPVETIETTIVGEEEEDDDEDDDEDGGGGDHGGGGGH-GHAGHHHHHHHHHH
MASGDTLYIATDGSEMPAEIVELHEIEVETIPVETIETTIVGEEEEDDDEDDDEDGGGGDHGGGGGH-GHAGHHHHHHHHHH
MASGDTLYIATDGSEMPAEIVELHEIEVETIPVETIETTIVGEEEEEDDDDEDGGGGDHGGGGGH-GHAGHHHHHHHHHH

--PPMIALQPLVTDDPTQVHHHQEVILVQTREEVVGDDSDGLRAEDGFEDQILIPVPAPAGGDDDYIEQTLVTVAAAGK
--PPMIALQPLVTDDPTQVHHHQEVILVQTREEVVGDDSDGLRAEDGFEDQILIPVPAPAGGDDDYIEQTLVTVAAAGK
HHPPMIALQPLVTDDPTQVHHHQEVILVQTREEVVGDDSDGLRAEDGFEDQILIPVPAPAGGDDDYIEQTLVTVAAAGK

SGGGSSSGGGRVKKGGGKSGKKSYLEGSGAGAAGGGGADPGNKKWEQKQVQIKTLEGEFSVTMWSSDEKKDIDHETVVEE
SGGGSSSGGGRVKKGGGKSGKKSYLEGSGAGAAGGGGADPGNKKWEQKQVQIKTLEGEFSVTMWSSDEKKDIDHETVVEE
SGGGAASSGGGRVKKGGGKSGKKSYLEGSGAGAAGGGGADPGNKKWEQKQVQIKTLEGESVTMWSSDEKKDIDHETVVEE

QIIGENSPPDYSEYMTGKKLPPGGIPGIDLSDPKQLAEFARMKPRKIKEDDAPRTIA
QIIGENSPPDYSEYMTGKKLPPGGIPGIDLSDPKQLAEFARMKPRKIKEDDAPRTIA
QIIGENSPPDYSEYMTGKKLPPGGIPGIDLSDPKQLAEFARMKPRKIKEDDAPRTIA

*Zinc finger

CPHKGCTKMFRDNSAMRKHLHHTHGPRVHVCAECGKAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVRIH
CPHKGCTKFRDNSAMRKHLHHTHGPRVHVCAECGKAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVRIH
CPHKGCTKMFRDNSAMRKHLHHTHGPRVHVCAECGKAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVGIH

Zinc finger*

TGDRPYVCPFDGCNKKFAQSTNLKSHILTH
TGDRPYVCPFDGCNKKFAQSTNLKSHILTH
TGDRPYVCPFDGCNKKFAQSTNLKSHILTH

AKAKNNQ*

AKAKNNQ*

AKAKNNQ*

n=411/414

Figure 11

YY1 primers

Designation	Position	Primer sequences
K823-F (Promotor)		CAC AGG CGT TTC TCG TCA GAG
K825-R (Promotor)		AAT ACC AAC TCC TCA ACC CCG A
K884-F	-104	CTT CCT CCC TCT GCC TTC CTT
K801-F	55-75	GAG ATC GTG GAA CTG CAT GAG
K827-R	127-150	GTC TTC GTC GTC GTC CTC CTC CTC
K814-F	417-437	CGG AGA CGA CGA CTA CAT CGA
K806-R	428-452	GTG ACC AGC GTC TGC TCG ATG TAG T
K804-R	529-550	CCA GGT AAC TCT TCT TGC CGC
K805-R	589-610	G TT CCC ACT TCT TAT TAC CCG G
K828-F	627-648	CAA GAC CCT GGA GGG CGA GTT C
K830-F	697-721	ACA GTG GTT GAA GAG CAG ATC ATT G
K829-R	690-722	CCA ATG ATC TGC TCT TCA ACC AC
K831-F	839-866	GCC AAG AAA AAT TAA AGA AGA TGA TGC
K832-R	856-881	GCT ATT GTT CTT GGA GCA TCA TCT TC
K815-F	997-1021	GAG AGC TCA AAG CTA AAA CGA CAC C
K833-R	1026-1050	AAA GGG CTT TTC TCC AGT ATG AAC C
K817-R	1077-1099	AAT TGA AGT CCA GTG AAA AGG GC
K816-F	1105-1126	ACG CAT GTG CGA ATC CAT ACC G
K870-R	1346-1372	CAA AAC ATG TCC CTT AAG TGT GTA GGA
K818-R	1501-1528	AAT TGT AAG CAA CAG GTG AGC TTC ATG
K821-F (Intron 3)		GCG AAG CAC CCC CAC ACT AAA TTT C
K874-F (Intron 3)		GCT TAT AAG TGC TGT TGG CTA CAG CT
K875-R (Intron 3)		GTC ACC TGG AGC TGT AGC CAA C

F1	10	1	TCACTGGACTTCAATTTGCGC	(1084)
F2	12	1	TTTTCACTGGACTTCAATTTGCG	(1081)
F3	12	1	ACCAGATCCTCATTCGGTACC	(383)
F4	14	1	CCCTTTCAGTGCACATTCGAA	(1045)
F5	15	1	GACGACGAAGACGACGAGGAT	(139)
F6	17	1	GAGAGCTCAAAGCTAAAACGACACC	(997)
F7	19	1	GGAGACGACGACTACATCGAGC	(418)
F8	22	1	CGGAGACGACGACTACATCGA	(417)
F9	23	1	TGAGAGCTCAAAGCTAAAACGACAC	(996)
F10	24	1	GAGGACCAGATCCTCATTCGG	(379)
F11	26	1	AACTCCCTCCTGGAGGGATACC	(767)
F12	27	1	GAGACGACGACTACATCGAGCAG	(419)
F13	29	2	GAGGAGGACGACGACGAAGAC	(130)
F14	30	1	TTGAGAGCTCAAAGCTAAAACGACA	(995)
F15	30	1	ACCCTCTACATTGCCACGGAC	(16)
F16	30	1	ACTACATCGAGCAGACGCTGGT	(428)
F17	34	1	GAGCTCAAAGCTAAAACGACACCA	(999)
F18	35	1	TTCAGTGCACATTCGAAGGCT	(1049)
F19	36	2	TGGAGACTATCGAGACCACGGT	(98)
F20	37	1	TTTCAGTGCACATTCGAAGGC	(1048)
F21	39	1	GTGCGAATCCATACCGGAGAC	(1111)
F22	41	1	GAGGTGATTCTGGTGCAGACG	(301)
F23	41	1	ACTCCCTCCTGGAGGGATACCT	(768)
F24	41	2	GTGGAGACTATCGAGACCACGG	(97)
F25	41	1	AGAGGTGATTCTGGTGCAGACG	(300)
F26	42	1	TGAAATCTCACATCTTAACACACGCT	(1190)
F27	43	2	TACATCGAGCAGACGCTGGTC	(430)
F28	43	1	ACGACTACATCGAGCAGACGCT	(425)
F29	43	1	GAAACTCCCTCCTGGAGGGATAC	(765)
F30	49	1	CTGCACAAAGATGTTTCAGGGATAAC	(897)

Figure 11 - 1. Continued

F31	52	1	AAAACGACACCAGCTGGTTCATAC	(1011)
F32	52	1	TAAAACGACACCAGCTGGTTCATAC	(1010)
F33	53	1	AGAAGAGCGGCAAGAAGAGTTACC	(524)
F34	53	1	ACCTGAAATCTCACATCTTAACACACG	(1187)
F35	53	1	CCTGAAATCTCACATCTTAACACACG	(1188)
F36	55	1	GACACCAGCTGGTTCATACTGGA	(1016)
F37	55	2	GGTGGAGACTATCGAGACCACG	(96)
F38	55	1	AGACGACGACTACATCGAGCAGA	(420)
F39	57	1	CAGTGGTTGAAGAGCAGATCATTG	(698)
F40	57	1	ACAGTGGTTGAAGAGCAGATCATTG	(697)
F41	57	1	GGTTGAAGAGCAGATCATTGGG	(702)
F42	58	1	GGTCCAGAGTCCACGTCTGT	(952)
F43	59	1	TGCACAAAGATGTTTCAGGGATAACT	(898)
F44	60	1	GATGCTCCAAGAACAATAGCTTGC	(862)
F45	62	1	GTCCAGAGTCCACGTCTGTG	(953)
F46	67	1	GCTTTTCACTGGACTTCAATTTGC	(1079)
F47	67	1	AGTGGTTGAAGAGCAGATCATTGG	(699)
F48	67	1	GTGGTTGAAGAGCAGATCATTGG	(700)
F49	71	1	AGAGCGGCAAGAAGAGTTACCTG	(527)
F50	71	1	TCACATCTTAACACACGCTAAAGCC	(1197)
F51	72	1	ATCTCACATCTTAACACACGCTAAAGC	(1194)
F52	73	1	CTGAAATCTCACATCTTAACACACGC	(1189)
F53	74	1	ACGACACCAGCTGGTTCATACTG	(1014)
F54	76	1	AGATATTGACCATGAAACAGTGGTTGA	(681)
F55	76	1	GATATTGACCATGAAACAGTGGTTGA	(682)
F56	76	1	GAGGGATACCTGGCATTGACCT	(779)
F57	77	1	AGACCATCCCGGTGGAGACTAT	(86)
F58	78	1	GAAGAGCGGCAAGAAGAGTTACCT	(525)
F59	78	3	GGAGACTATCGAGACCACGGTG	(99)
F60	82	1	GGTTCGAGGACCAGATCCTCA	(374)
F61	83	2	GAGCAGATCATTGGGGAGAATC	(709)
F62	87	1	GAAGATGATGCTCCAAGAACAATAGC	(856)
F63	88	1	CGCTAAAGCCAAAAACAACCAGT	(1212)
F64	88	1	ATACCGGAGACAGGCCCTATGT	(1121)
F65	89	1	CAATAGCTTGCCCTCATAAAGGC	(875)
F66	89	1	AAGATATTGACCATGAAACAGTGGTTG	(680)
F67	89	1	ACAATAGCTTGCCCTCATAAAGGC	(874)
F68	92	1	AGAAAAGCCCTTTCAGTGCACA	(1038)
F69	95	1	ATATTGACCATGAAACAGTGGTTGAAG	(683)
F70	95	1	GCGGCAAGAAGAGTTACCTGG	(530)
F71	95	1	TATTGACCATGAAACAGTGGTTGAAG	(684)
F72	95	1	ATTGACCATGAAACAGTGGTTGAAG	(685)
F73	95	1	TTGACCATGAAACAGTGGTTGAAG	(686)
F74	96	1	GAACAATAGCTTGCCCTCATAAAGG	(872)
F75	96	1	AGAACAATAGCTTGCCCTCATAAAGG	(871)
F76	98	1	ACCTCTCAGACCCCAAGCAACT	(797)
F77	99	1	ACGCTAAAGCCAAAAACAACCAG	(1211)
F78	101	1	AAGATGATGCTCCAAGAACAATAGCTT	(857)
F79	101	1	AAACGACACCAGCTGGTTCATACT	(1012)
F80	102	1	CGACGGTTGTAATAAGAAGTTTGCTC	(1152)
F81	103	1	CAAGAACAATAGCTTGCCCTCATAAA	(869)
F82	103	1	GGAACAGAAGCAGGTGCAGATC	(606)
F83	106	1	AAAAGCCCTTTCAGTGCACATTC	(1040)
F84	106	2	TCTGCTATGAGAAAGCATCTGCAC	(922)
F85	106	1	AAACAGTGGTTGAAGAGCAGATCATT	(695)
F86	106	1	TTCGACGGTTGTAATAAGAAGTTTGC	(1150)
F87	106	1	AGCGTTTCGTTGAGAGCTCAAAG	(987)
F88	106	1	GCCCCCTCGACGGTTGTAATA	(1145)
F89	107	1	CAACTGGCAGAATTTGCCAGA	(814)
F90	107	1	AGTTCTCGGTCACCATGTGGTC	(644)
F91	108	1	TGAGAAAGCATCTGCACACCC	(929)

Figure 11 - 2. Continued

F92	108	1	ATGAGAAAGCATCTGCACACCC	(928)
F93	108	1	TATGAGAAAGCATCTGCACACCC	(927)
F94	111	1	GAGTTCTCGGTCACCATGTGGT	(643)
F95	111	1	CACCACCACCAAGAGGTGATTC	(289)
F96	111	1	GACGACGACTACATCGAGCAGAC	(421)
F97	112	1	CCCGGTGGAGACTATCGAGAC	(93)
F98	112	1	CAGAAGCAGGTGCAGATCAAGAC	(610)
F99	112	1	GCTAAAGCCAAAAACAACCAGTGA	(1213)
F100	113	1	GACCTCTCAGACCCCAAGCAA	(796)

R1	3	1	GCAAACCTTCTTATTACAACCGTCGAA	(1175)
R2	4	1	ACATAGGGCCTGTCTCCGGTAT	(1142)
R3	4	1	AGCAAACCTTCTTATTACAACCGTCGA	(1176)
R4	6	1	AGCTTTGAGCTCTCAACGAACG	(1010)
R5	8	1	GAGCAAACCTTCTTATTACAACCGTCG	(1177)
R6	8	1	CTTTGAGCTCTCAACGAACGCT	(1008)
R7	9	1	GGTTGTTTTTGGCTTTAGCGTGT	(1231)
R8	10	1	CTGGTTGTTTTTGGCTTTAGCGT	(1233)
R9	11	1	CCTGTCTCCGGTATGGATTCTG	(1134)
R10	12	1	CTGTCTCCGGTATGGATTCTGC	(1133)
R11	12	1	GTCTCCGGTATGGATTCTGCAC	(1131)
R12	12	1	AGCGTCTGCTCGATGTAGTCGT	(446)
R13	13	1	TTCTGTTCCCACTTCTTATTACCCG	(614)
R14	15	2	TCTGCTCGATGTAGTCGTCTCT	(442)
R15	15	1	ACTGGTTGTTTTTGGCTTTAGCG	(1234)
R16	16	4	GTCTGCTCGATGTAGTCGTCTCT	(443)
R17	16	4	ATCCTCGTCTCTTCGTCTCT	(159)
R18	17	1	CAGTAGAACCAGCTGGTGTCGT	(1036)
R19	17	1	TTGAGCTCTCAACGAACGCTTT	(1006)
R20	19	1	AGACCACATGGTGACCGAGAAC	(666)
R21	19	1	CTTCTTATTACCCGGGTCGGC	(603)
R22	20	1	CTGCTCGATGTAGTCGTCTCT	(441)
R23	21	1	TCGATGTAGTCGTCTCTCCG	(437)
R24	22	1	TTTGAGCTCTCAACGAACGCTT	(1007)
R25	22	1	CCACTTCTTATTACCCGGGTCG	(606)
R26	22	1	CACTTCTTATTACCCGGGTCGG	(605)
R27	22	1	GACCAGCTCTGCTCGATGTA	(450)
R28	23	1	AATTGAAGTCCAGTGAAAAGCGC	(1099)
R29	23	1	TGAACCAGCTGGTGTCGTTTTAG	(1031)
R30	23	1	GACCACATGGTGACCGAGAACT	(665)
R31	25	1	AACTTCTTATTACAACCGTCGAAGGG	(1172)
R32	25	1	TGTTCCCACTTCTTATTACCCGG	(611)
R33	26	3	CCCAGGTAACCTCTTCTTGCCG	(551)
R34	26	1	AGAGGTCAATGCCAGGTATCCC	(802)
R35	26	2	CCAGGTAACCTCTTCTTGCCGC	(550)
R36	27	1	TTGAAGTCCAGTGAAAAGCGCT	(1097)
R37	29	1	TGAGGATCTGGTCCCTCGAACC	(394)
R38	29	1	CACATGGTGACCGAGAACTCG	(662)
R39	29	1	GTATGAACCAGCTGGTGTCGTTTT	(1034)
R40	30	1	TCAATCTCATGCAGTTCACGAT	(80)
R41	30	1	TCAATCTCATGCAGTTCACGA	(80)
R42	30	1	AGTATGAACCAGCTGGTGTCGTTT	(1035)
R43	32	1	GGTCTCGATAGTCTCCACCGG	(114)
R44	33	1	AAGACCACATGGTGACCGAGAA	(667)
R45	33	1	CAATCTCATGCAGTTCACGATC	(79)
R46	34	1	GGAATGAGGATCTGGTCCCTCG	(398)
R47	34	2	TTCCCACTTCTTATTACCCGGGT	(609)
R48	34	2	TGAAGTCCAGTGAAAAGCGCTT	(1096)
R49	35	1	GCTCGATGTAGTCGTCTCTCC	(439)

Figure 11 - 3. Continued

R50	36	1	GTATGAACCAGCTGGTGTCTGTTTTA	(1034)
R51	36	1	TTCCCACTTCTTATTACCCGGG	(609)
R52	42	1	GAATGAGGATCTGGTCCCTCGAAC	(397)
R53	43	1	GAGGTCAATGCCAGGTATCCCT	(801)
R54	44	1	GTGGTCTCGATAGTCTCCACCG	(116)
R55	44	1	AGGTAACCTCTTCTTGCCGCTCTTC	(548)
R56	45	1	CACATTCTGCACAGACGTGGA	(982)
R57	46	1	AAAGGGCTTTTCTCCAGTATGAACC	(1050)
R58	47	2	ACCATCCTCGTCGTCTTCGTC	(162)
R59	48	1	GCTTCTGTTCCTTCTTATTACCC	(616)
R60	48	1	CACATTCTGCACAGACGTGGAC	(982)
R61	49	1	CAGGTAACCTCTTCTTGCCGCTCT	(549)
R62	49	1	GATGCTTTCTCATAGCAGAGTTATCCC	(940)
R63	49	1	CTGAAGACCACATGGTGACCG	(670)
R64	50	2	CCTGCTTCTGTTCCTTCTTATTAC	(619)
R65	52	1	ACCAGCGTCTGCTCGATGTAGT	(449)
R66	53	1	TCTTATTACAACCGTCAAGGGG	(1168)
R67	53	1	TTGTTTTTGGCTTTAGCGTGTGT	(1229)
R68	54	1	ACTGAAAGGGCTTTTCTCCAGTATG	(1054)
R69	55	1	CACGTAAAGGGCTTTTCTCCAGTAT	(1055)
R70	57	1	GAGGTGAGTTCTCCCAATGATC	(736)
R71	58	1	GGTACCGGAATGAGGATCTGGT	(404)
R72	62	1	GTCTCGATAGTCTCCACCGGG	(113)
R73	63	1	CTTCAACCACTGTTTCATGGTCAATA	(709)
R74	64	1	CCTTTATGAGGGCAAGCTATTGTTC	(896)
R75	64	1	CTTCAACCACTGTTTCATGGTCAATAT	(709)
R76	65	1	TTTTTGGCTTTAGCGTGTGTTAAGAT	(1226)
R77	66	1	TTGTTTTTGGCTTTAGCGTGTGTTA	(1229)
R78	69	1	CTTGGGGTCTGAGAGGTCAATG	(813)
R79	71	1	GTCCGTGGCAATGTAGAGGGT	(36)
R80	71	1	TCTGGCAAATTCTGCCAGTTG	(834)
R81	72	1	TCACTGGTTGTTTTTGGCTTTAGC	(1236)
R82	72	1	CTTTGTGCAGCCTTTATGAGGG	(906)
R83	73	1	GTTGTTTTTGGCTTTAGCGTGTGT	(1230)
R84	74	1	TGAAAGGGCTTTTCTCCAGTATGA	(1052)
R85	75	1	GCAAGCTATTGTTCTTGGAGCATC	(885)
R86	76	1	GCCTTTATGAGGGCAAGCTATTG	(897)
R87	76	1	GCTTGGGGTCTGAGAGGTCAAT	(814)
R88	76	1	CCAATGATCTGCTCTTCAACCAC	(722)
R89	77	1	CCACCGTGGTCTCGATAGTCTC	(121)
R90	78	1	CTGCTTCTGTTCCCACTTCTTATTACC	(618)
R91	80	1	TTGGCTTCATTCTGGCAAATTC	(844)
R92	81	1	CTTCAACCACTGTTTCATGGTCAAT	(709)
R93	81	1	AATCTCATGCAGTCCACGATCTC	(78)
R94	82	1	CTTCAACCACTGTTTCATGGTCAA	(709)
R95	83	1	GGGCTTTTCTCCAGTATGAACCA	(1047)
R96	83	2	ACCACATGGTGACCGAGAACTC	(664)
R97	84	1	GTGCAGATGCTTTCTCATAGCAGA	(945)
R98	84	1	TGTGCAGATGCTTTCTCATAGCAG	(946)
R99	85	1	CATTCTGCACAGACGTGGACTC	(980)
R100	85	1	TCTGAGAGGTCAATGCCAGGTATC	(806)

Figure 12

Shortened zinc finger of BB.6S

1. Nucleic acid sequence of the "shortened" zinc finger for BB.6S (the nucleotides that are crossed out are absent, only the underlined nucleotides code for amino acids of the protein in the second band)

```
1  ATGGCCTCGG GCGACACCTT CTACATTGCC ACGGACGGCT CGGAGATGCC
51  AGCCGAGATC GTGGAAGTGC ATGAGATTGA GGTGGAGACC ATCCCGGTGG
101 AGACTATCGA GACCACGGTG GTGGGCGAGG AGGAGGACGA CGACGAAGAC
151 GACGAGGATG GTGGCGGCGG AGACCACGGT GGCGGGGGCG GCCACGGGCA
201 CGCTGGCCAC CACCATCACC ACCACCACCA CCACCACCCG CCCATGATCG
251 CGCTGCAGCC GCTGGTCACC GACGACCCGA CCCAAGTGCA CCACCACCAA
301 GAGGTGATTC TGGTGCAGAC GCGCGAGGAG GTAGTGGGTG GCGACGACTC
351 GGACGGGCTG CGCGCCGAGG ACGGGTTCGA GGACCAGATC CTCATTCCGG
401 TACCCGCGCC GGCCGGCGGA GACGACGACT ACATCGAGCA GACGCTGGTC
451 ACCGTGGCGG CGGCCGGCAA GAGCGGTGGC GGTCTTCGT CGGGCGGCGG
501 CCGCGTTAAG AAGGGCGGCG GCAAGAAGAG cGGCAAGAAG AGTTACCTGG
551 GCAGCGGGGC CGGCGCGGCG GCGGTGGCG GCGCCGACCC GGGTAATAAG
601 AAGTGGGAAc AGAAGCAGGT GCAGATCAAG ACCCTGGAGG GCGAGTTCTC
651 GGTCAACATG TGGTCTTCAG ATGAAAAAAA AGATATTGAC CATGAAACAG
701 TGGTTGAAGA GCAGATCATT GGGGAGAACT CACCTCCTGA TTATTCTGAA
751 TATATGACAG GCAAGAAACT CCCTCCTGGA GGGATACCTG GCATTGACCT
801 CTCAGACCCC AAGCAACTGG CAGAATTTGC CAGAATGAAG CCAAGAAAAA
851 TTAAAGAAGA TGATGCTCCA AGAACAATAG CTTGCCCTCA TAAAGGCTGG
901 ACAAAGATGT TCAGGCATAA CTCTGGTATG AgAAAGCATC TGCACACCGA
951 CGGTCCCAGA GTCCACGTCT GTGCAGAAATG TGGCAAAGCG TTCCTTGACA
1001 GCTCAAAGCT AAAACGACAC CAGCTGGTTC ATACTGCAGA AAAGCCCTTT
1051 CAGTGCACAT TCGAAGGCTG CGGGAAGCGC TTTTCACTGG ACTTCAATTT
1101 GCGCACGCAT GTGCGAATCC ATACCGGAGA CAGGCCCTAT GTGTGCCCTT
1151 TCGACGGTTG TAATAAGAAG TTTGCTCAGT CAACTAACCT GAAATCTCAC
1201 ATCTTAACAC ACGCTAAAGC CAAAAACAAC CAGTGA
```

2. Protein sequence of the "shortened" zinc finger for BB.6S (the nucleotides that are crossed out are absent, only the underlined nucleotides are present in the second band)

```
CPHK G C T K M F R D N S A M R K H L H T H G P R V H V  
C A E C G K A F V E S S K L K R H Q L V H T G E K P F Q  
CTFEGCGKRFSLDENLRTHVRIHTGDRPYV  
CPFDGCNKKFAQSTNLKSHILTH
```

Figure 13

Antisense oligonucleotides used in accordance with the present invention

(The positions given relate to the coding region and not to the position numbering of the sequence listing.)

>gi|1835104|emb|Z85393.1|HSZ85393 H.sapiens Ig lambda light chain variable region gene(34-30SWIIE197) rearranged; Ig-Light-Lambda; VLambda
Identities = 14/14 (100%)

Query: 74 accggagcccgtg 88
|||||
Sbjct: 241 accggagcccgtg 228
V_region 1..348

>gi|14589948|ref|NM_000937.2| Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA
Identities = 17/18 (94%)

Query: 77 ggagcccgtgtgggaga 94
|||||
Sbjct: 5099 ggagcccgtgtgtgggaga 5082
CDS 387..6299

>gi|18596386|ref|XM_093190.1| Homo sapiens similar to T-cell activation protein (LOC170226), mRNA
Identities = 20/21 (95%)

Query: 76 cggagcccgtgtgtgggagatg 96
|||||
Sbjct: 156 cggagcacgtgtgtgtgggagatg 176
CDS 1..1314

>gi|7934571|gb|AF220152.2|AF220152 Homo sapiens TACC2 mRNA, complete cds
Identities = 14/14 (100%)

Query: 78 gagcccgtgtgtggg 91
|||||
Sbjct: 977 gagcccgtgtgtgtggg 990
CDS 293..3013

>gi|6165844|gb|AF100772.1|AF100772 Homo sapiens tenascin-M1 (TNM1) mRNA,
Identities = 16/16 (100%)

Query: 79 agcccgtgtgtgggaga 94
|||||
Sbjct: 4377 agcccgtgtgtgtgggaga 4362
CDS 65..8242
function="putative receptor molecule"

>gi|24496766|ref|NM_004712.3| Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate (HGS), mRNA
Identities = 15/15 (100%)

Query: 79 agcccgtgtgtgggag 93
|||||
Sbjct: 2088 agcccgtgtgtgtgggag 2074

CDS 78..2411
 /note="human growth factor-regulated tyrosine kinase
 >gi|4324953|gb|AF114821.1|HSSMO3 Homo sapiens smoothened (SMO) gene, exons 3
 through 12 and complete
 Identities = 14/14 (100%)

Query: 79 agcccgctgtggga 93
 |||||
 Sbjct: 6838 agcccgctgtggga 6825
 CDS 6833..6967

>gi|22064913|ref|XM_090047.5| Homo sapiens LOC160156 (LOC160156), mRNA
 Identities = 14/14 (100%)

Query: 80 gcccgctgtgggag 93
 |||||
 Sbjct: 1427 gcccgctgtgggag 1440
 CDS 709..1980

>gi|517388|emb|Z31606.1|HSB2NO3 H.sapiens brain-2/N-Oct 3 gene (promoter
 region)
 Identities = 15/15 (100%)

Query: 80 gcccgctgtgggaga 94
 |||||
 Sbjct: 547 gcccgctgtgggaga 561
 promoter 1..670
 >gi|23273501|gb|BC035782.1| Homo sapiens, Similar to tyrosine kinase, non-
 receptor, 1, clone
 Identities = 15/15 (100%)

Query: 83 cgctgtgggagatgt 97
 |||||
 Sbjct: 1032 cgctgtgggagatgt 1046
 CDS 98..2083

>gi|7662017|ref|NM_015153.1| Homo sapiens PHD finger protein 3 (PHF3), mRNA
 Identities = 14/14 (100%)

Query: 84 gctgtgggagatgt 97
 |||||
 Sbjct: 2228 gctgtgggagatgt 2241
 CDS 28..6147
 >gi|20561197|ref|XM_062302.3| Homo sapiens similar to RING finger protein 18
 (Testis-specific ring-finger protein) (LOC120826), mRNA
 Score = 28.2 bits (14), Expect = 119
 Identities = 14/14 (100%)

Query: 84 gctgtgggagatgt 97
 |||||
 Sbjct: 489 gctgtgggagatgt 502
 CDS 190..2244
 /product="similar to RING finger protein 18(Testis-specific ring-finger rotein)"
 >gi|4885330|ref|NM_005305.1| Homo sapiens G protein-coupled receptor 42
 (GPR42), mRNA
 Identities = 14/14 (100%)

Query: 84 gctgtgggagatgt 97
 |||||
 Sbjct: 486 gctgtgggagatgt 473
 CDS 1..1041
 >gi|17473297|ref|XM_061928.1| Homo sapiens LOC120226 (LOC120226), mRNA

Identities = 14/14 (100%)

Query: 84 gctgtgggagatgt 97
|||||
Sbjct: 453 gctgtgggagatgt 466
CDS 1..492

>gi|21359977|ref|NM_024947.2| Homo sapiens polyhomeotic like 3 (Drosophila)
(PHC3), mRNA
Identities = 14/14 (100%)

Query: 85 ctgtgggagatgta 97
|||||
Sbjct: 404 ctgtgggagatgta 391
CDS 65..2959
/note="early development regulator 3; polyhomeotic 3"

>gi|19718811|gb|BC007249.2| Homo sapiens, pelota homolog (Drosophila), clone
Identities = 13/13 (100%)

Query: 97 taacggtgcctgc 109
|||||
Sbjct: 1303 taacggtgcctgc 1291
CDS 274..1431
/product="pelota homolog (Drosophila)"

>gi|19924298|ref|NM_004958.2| Homo sapiens FK506 binding protein 12-rapamycin
associated protein 1 (FRAP1), mRNA
Identities = 13/13 (100%)

Query: 98 acggtgcctgccg 111
|||||
Sbjct: 5720 acggtgcctgccg 5732
CDS 80..7729
/note="FK506 binding protein 12-rapamycin associated protein 2; rapamycin target
protein; FKBP12-rapamycin complex-associated protein 1; FKBP-rapamycin
associated"

>gi|22049727|ref|XM_040948.8| Homo sapiens dynein, cytoplasmic, heavy
polypeptide 1 (DNCH1), mRNA
Identities = 13/13 (100%)

Query: 99 acggtgcctgccg 111
|||||
Sbjct: 6291 acggtgcctgccg 6303
CDS 6..6830
/product="similar to cytoplasmic dynein heavy chain"

>gi|459833|gb|L25085.1|HUMSEC61B Human Sec61-complex beta-subunit mRNA,
Identities = 14/14 (100%)

Query: 100 cggtgcctgccgag 113
|||||
Sbjct: 220 cggtgcctgccgag 207
CDS 64..354
/function="protein translocation across the er-membrane"

>gi|21704280|ref|NM_020433.2| Homo sapiens junctophilin 2 (JPH2), mRNA
Identities = 17/18 (94%)

Query: 100 cggcgcctgccgagcctc 117
 |||||
 Sbjct: 2526 cggcgcctgcagagcctc 2509
 CDS 874..2964
 mediate cross talk between cell surface and intracellular ion channels.

>gi|12804622|gb|BC001734.1|BC001734 Homo sapiens, protein translocation complex beta, clone MGC:1255
 Identities = 14/14 (100%)

Query: 100 cggcgcctgccgag 113
 |||||
 Sbjct: 233 cggcgcctgccgag 220
 CDS 77..367
 >gi|22053428|ref|XM_038146.5| Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA
 Identities = 16/17 (94%)

Query: 100 cggcgcctgccgagcct 116
 |||||
 Sbjct: 289 cggcgcctgccgagcct 305
 CDS 74..826
 /product="similar to Gamma-interferon inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30)"

>gi|7657145|ref|NM_014365.1| Homo sapiens protein kinase H11 (H11), mRNA
 Identities = 13/13 (100%)

Query: 101 ggtgcctgccgag 113
 |||||
 Sbjct: 763 ggtgcctgccgag 775
 CDS 524..1114
 /note="contains hsp20/crystallin family domain; estradiol-induced; small stress protein-like protein HSP22"
 >gi|21264316|ref|NM_014599.3| Homo sapiens melanoma antigen, family D, 2 (MAGED2), mRNA
 Identities = 17/18 (94%)

Query: 101 ggtgcctgccgagcctct 118
 |||||
 Sbjct: 332 ggtgcctcccgagcctct 315
 CDS 97..1917
 /note="hepatocellular carcinoma associated protein; breast cancer associated gene 1"
 >gi|11967745|emb|AJ293618.1|HSA293618 Homo sapiens mRNA for hypothetical protein 11B6, clone XP11B6
 Identities = 17/18 (94%)

Query: 101 ggtgcctgccgagcctct 118
 |||||
 Sbjct: 248 ggtgcctcccgagcctct 231
 CDS 13..1833
 >gi|20514781|ref|NM_139015.1| Homo sapiens SPPL3 (SPPL3), mRNA
 Identities = 14/14 (100%)

Query: 104 gcctgccgagcctc 117
 |||||
 Sbjct: 569 gcctgccgagcctc 582
 CDS 1..1905
 /product="hypothetical protein XP_068909"

>gi|23094385|emb|AJ345030.1|HSA345030 Homo sapiens mRNA for presenilin-like protein 4 (PSL4 gene)
Identities = 14/14 (100%)

Query: 104 gcctgccgagcctc 117
|||||
Sbjct: 598 gcctgccgagcctc 611
CDS 54..1208
/function="putative intramembrane protease"

>gi|4502840|ref|NM_003654.1| Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA
Identities = 16/17 (94%)

Query: 105 cctgccgagcctctacg 121
|||||
Sbjct: 735 cctgccgagcctctacg 751
CDS 367..1602
/note="carbohydrate (chondroitin 6/keratan) sulfotransferase 1"
/protein_id="NP_003645.1"

>gi|17485022|ref|XM_066361.1| Homo sapiens similar to glutathione S-transferase theta 1 (LOC129041), mRNA
Identities = 13/13 (100%)

Query: 105 cctgccgagcctc 117
|||||
Sbjct: 580 cctgccgagcctc 568
CDS 1..633
/product="similar to glutathione S-transferase theta 1"

>gi|22134527|gb|AF331523.1| Homo sapiens chromosome 12 putative anion transporter mRNA, partial
Identities = 13/13 (100%)

Query: 106 ctgccgagcctct 118
|||||
Sbjct: 807 ctgccgagcctct 819
CDS <312..2003
note="member of the SLC26 family;

>gi|14784297|ref|XM_031102.1| Homo sapiens Breakpoint cluster region protein, uterine leiomyoma, 2 (BCRP2), mRNA
Identities = 13/13 (100%)

Query: 108 gccgagcctctac 120
|||||
Sbjct: 1784 gccgagcctctac 1796
CDS 55..2883
/product="similar to KIAA1824 protein"

>gi|20535791|ref|XM_119632.1| Homo sapiens LOC205318 (LOC205318), mRNA
Identities = 14/14 (100%)

Query: 123 tcggctctagcacc 136
|||||
Sbjct: 491 tcggctctagcacc 504
CDS 1..522
/product="hypothetical protein XP_119632"

>gi|4557448|ref|NM_001271.1| Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2), mRNA
Identities = 14/14 (100%)

Query: 125 ggctctagcacctt 138
|||||
Sbjct: 2791 ggctctagcacctt 2778
CDS 708..5927
/product="chromodomain helicase DNA binding protein 2"

>gi|21264574|ref|NM_139135.1| Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1), transcript variant 2, mRNA
Identities = 14/14 (100%)

Query: 128 tctagcaccttgac 141
|||||
Sbjct: 5474 tctagcaccttgac 5487
CDS 371..6577
/note="brain protein 120; chromosome 1 open reading frame 4; SWI/SNF complex protein p270; BRG1-associated factor 250a; chromatin remodeling factor p250; OSA1 nuclear protein"

>gi|18129612|gb|AF333072.2|AF333072 Homo sapiens HERV-K18.1 5' long terminal repeat, complete sequence; gag protein (gag) gene, gag-K18.1 allele, complete cds; pol protein (pol) gene, pol-K18.1 allele, complete cds; env protein (env) gene, env-K18.1 allele, complete cds; and 3' long terminal repeat, complete sequence
Identities = 17/18 (94%)

Query: 143 tactctaactccacctct 160
|||||
Sbjct: 1196 tactctaactccccctct 1179
CDS 1113..1874
>gi|4503778|ref|NM_002029.1| Homo sapiens formyl peptide receptor 1 (FPR1),
Identities = 14/14 (100%)

Query: 148 taactccacctctg 161
|||||
Sbjct: 1102 taactccacctctg 1089
CDS 62..1114
/product="formyl peptide receptor 1"
/product="protein tyrosine kinase-7"
>gi|21655145|gb|AY082886.1| Homo sapiens eukaryotic translation initiation factor 4GI (EIF4GI)
Identities = 14/14 (100%)

Query: 150 actccacctctggt 163
|||||
Sbjct: 1400 actccacctctggt 1387
CDS 275..5077
>gi|13357213|ref|NM_015545.1| Homo sapiens KIAA0632 protein (KIAA0632), mRNA
Identities = 17/18 (94%)

Query: 152 tccacctctggtagggcc 169
|||||
Sbjct: 931 tccacctctggtagggcc 914
CDS 282..1790
/product="KIAA0632 protein"

>gi|18182862|gb|BC015632.1| Homo sapiens, similar to hypothetical protein
XP_166541, clone
Identities = 18/19 (94%)

Query: 153 ccacctctggtagggccac 171
||||||| |||||
Sbjct: 2098 ccacctcgggtagggccac 2080
CDS 52..2517

>gi|24432033|ref|NM_004959.3| Homo sapiens nuclear receptor subfamily 5, group
A, member 1 (NR5A1),
Identities = 17/18 (94%)

Query: 159 ctggtagggccacctctg 176
|||| |||||
Sbjct: 2316 ctgggagggccacctctg 2299
CDS 52..13776

>gi|17432414|gb|AF447167.1|F447157S05 Homo sapiens protein tyrosine kinase-7
(PTK7) gene, exons 11, 12, and 13
Identities = 15/15 (100%)

Query: 161 ggtagggccacctct 175
|||||
Sbjct: 553 ggtagggccacctct 567
CDS AF447164.1: 548..683

>gi|19882212|ref|NM_032119.1| Homo sapiens very large G protein-coupled
receptor 1 (VLGR1), mRNA
Identities = 17/18 (94%)

Query: 170 acctctgatagctctggt 187
|||||
Sbjct: 11300 acctctgataactctggt 11283
CDS 97..19020

>gi|22044294|ref|XM_174449.1| Homo sapiens LOC255281 (LOC255281), mRNA
Identities = 16/16 (100%)

Query: 180 cctctgatagctctgg 196
|||||
Sbjct: 460 cctctgatagctctgg 445
CDS 1..474

>gi|1841544|gb|U89337.1|HSMHC3W36A Homo sapiens HLA class III region
containing NG7, cAMP response element binding protein-related protein (CREB-RP),
and tenascin X genes,
Identities = 17/18 (94%)

Query: 180 gctctggtgccaccacc 197
|||||
Sbjct: 54778 gctctggtgcctccacc 54795
CDS 54566..54883

>gi|6164703|gb|AF167572.1|AF167572 Homo sapiens protein methyltransferase
(JBP1) mRNA, complete cds
Identities = 14/14 (100%)

Query: 181 ctctggtgccacca 194
 |||||
 Sbjct: 574 ctctggtgccacca 561
 CDS 92..2005
 /function="methylates histones H2A and H4 and myelin basic
 /product="protein methyltransferase"

gi|2323409|gb|AF015913.1|AF015913 Homo sapiens SKB1Hs mRNA, complete cds
 Identities = 14/14 (100%)

Query: 181 ctctggtgccacca 194
 |||||
 Sbjct: 483 ctctggtgccacca 470
 CDS 1..1914
 /note="homolog of fission yeast Skb1"

>gi|18490998|ref|NM_003882.2| Homo sapiens WNT1 inducible signaling pathway
 protein 1 (WISPL), transcript variant 1, mRNA
 Identities = 18/19 (94%)

Query: 181 ctctggtgccaccaccgc 199
 ||||| |||||
 Sbjct: 569 ctctggtgccccaccgc 587
 CDS 77..1180

>gi|14245731|dbj|AB051853.1| Homo sapiens ARHGAP9 gene for rho-GTPase
 activating protein, complete
 Identities = 15/15 (100%)

Query: 181 ctctggtgccaccac 195
 |||||
 Sbjct: 2013 ctctggtgccaccac 2027
 CDS 140..2335
 /function="regulating adhesion of hematopoietic cells to
 extracellular matrix"

>gi|16876446|ref|NM_054028.1| Homo sapiens acyl-malonyl condensing enzyme
 (AMAC), mRNA
 Identities = 14/14 (100%)

Query: 181 ctctggtgccacca 194
 |||||
 Sbjct: 220 ctctggtgccacca 233
 CDS 122..1138

>gi|18594399|ref|XM_092954.1| Homo sapiens similar to acidic protein rich in
 leucines (LOC164697), mRNA
 Identities = 14/14 (100%)

Query: 182 tctggtgccaccac 195
 |||||
 Sbjct: 721 tctggtgccaccac 734
 CDS 1..2454
 /product="similar to acidic protein rich in leucines"

>gi|20553841|ref|XM_031689.6| Homo sapiens MAX dimerization protein 5 (MGA),
 mRNA
 Identities = 14/14 (100%)

Query: 182 tctggtgccaccac 195
 |||||
 Sbjct: 463 tctggtgccaccac 476
 CDS 82..4773
 /product="similar to MAX-interacting protein"

>gi|18575418|ref|XM_100074.1| Homo sapiens LOC159480 (LOC159480), mRNA
 Identities = 14/14 (100%)

Query: 183 ctggtgccaccacc 196
 |||||
 Sbjct: 475 ctggtgccaccacc 488
 CDS 1..1425
 /product="hypothetical protein XP_100074"

>gi|6912511|ref|NM_012330.1| Homo sapiens monocytic leukemia zinc finger protein-related factor (MORF), mRNA
 Identities = 14/14 (100%)

Query: 183 ctggtgccaccacc 196
 |||||
 Sbjct: 1535 ctggtgccaccacc 1548
 CDS 316..6537
 /note="alternatively spliced; histone acetyltransferase"
 /product="monocytic leukemia zinc finger protein-related factor"

>gi|18032211|gb|AF217500.1|AF217500 Homo sapiens histone acetyltransferase MOZ2 (MOZ2) mRNA, complete cds
 Identities = 14/14 (100%)

Query: 183 ctggtgccaccacc 196
 |||||
 Sbjct: 1708 ctggtgccaccacc 1721
 CDS 489..6707
 /note="MYST family member; similar to MOZ"
 /product="histone acetyltransferase MOZ2"

>gi|24497588|ref|NM_139058.1| Homo sapiens aristaless related homeobox (ARX), mRNA
 Identities = 15/15 (100%)

Query: 185 ggtgccaccaccgc 199
 |||||
 Sbjct: 663 ggtgccaccaccgc 649
 CDS 1..1689

>gi|4758787|ref|NM_004551.1| Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA
 Identities = 14/14 (100%)

Query: 187 tgccaccaccgc 200
 |||||
 Sbjct: 675 tgccaccaccgc 662
 CDS 13..807

>product="bA171A24.1 (RAR-related orphan receptor B)" gene="RORB"/
 Identities = 27/29 (93%)

Query: 189 ccaccaccgctcctcctcctgctgctgc 217
 |||||
 Sbjct: 140523 ccaccaccaactcctcctcctgctgctgc 140551

CDS: 140352..>140970

>gi|23510326|ref|NM_015692.1| Homo sapiens alpha-2 macroglobulin family
protein VIP (VIP), mRNA
Identities = 21/22 (95%)

Query:195 cccgctcctcctcctgctgctg 216
||||||| |||||
Sbjct: 47 cccgctcctgctcctgctgctg 68
CDS 18..5675
/note="contains Kazal-type serine protease inhibitor domain"

>gi|21536391|ref|NM_007037.2| Homo sapiens a disintegrin-like and
metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8 (ADAMTS8),
Identities = 29/32 (90%)

Query: 196 ccgctcctcctcctgctgctgcttctgctgct 227
||||||| || |||||
Sbjct: 741 ccgctcctgctgctgctgctgctgctgctgctgct 772
CDS 708..3380

>gi|7382453|ref|NM_005199.3| Homo sapiens cholinergic receptor, nicotinic,
gamma polypeptide (CHRNA3), mRNA
Identities = 22/23 (95%)

Query:196 ccgctcctcctcctgctgctgct 218
||||| |||||
Sbjct: 19 ccgctgctcctcctgctgctgct 41
CDS 1..1563

>gi|17738306|ref|NM_006650.2| Homo sapiens complexin 2 (CPLX2), mRNA
Identities = 18/18 (100%)

Query: 197 cgctcctcctcctgctgc 214
|||||
Sbjct: 488 cgctcctcctcctgctgc 471
CDS 346..750

>gi|21362089|ref|NM_032667.2| Homo sapiens Bernardinelli-Seip congenital
lipodystrophy 2 (seipin) (BSCL2), mRNA
Identities = 24/26 (92%)

Query: 198 gctcctcctcctgctgctgcttctgc 224
||||| |||||
Sbjct: 1797 gctcctgctcctgcttctgcttctgc 1822
CDS 507..1901

>gi|21703365|ref|NM_022766.3| Homo sapiens ceramide kinase (CERK), mRNA
Identities = 21/22 (95%)

Query: 198 gctcctcctcctgctgctgctt 219
|||||
Sbjct: 1216 gctcctcctccagctgctgctt 1195

Identities = 14/14 (100%)

Query: 204 cctcctgctgctgc 217
|||||
Sbjct: 1586 cctcctgctgctgc 1599
CDS 124..1737
/note="lipid kinase LK4"

>gi|10198655|ref|NM_020547.1| Homo sapiens anti-Mullerian hormone receptor,
type II (AMHR2), mRNA
Identities = 20/20 (100%)

Query: 199 ctcctcctcctgctgctgct 218
|||||
Sbjct: 544 ctcctcctcctgctgctgct 563
CDS 79..1800

>gi|7662013|ref|NM_014745.1| Homo sapiens KIAA0233 gene product (KIAA0233),
mRNA
Identities = 30/32 (93%)

Query: 199 ctcctcctcctgctgctgcttctgctgctcct 230
|||||
Sbjct: 803 ctcctcctcctgctgctgctgctgatgctcct 772
CDS 3..6110

>gi|4504382|ref|NM_001528.1| Homo sapiens HGF activator (HGFAC), mRNA
Identities = 27/28 (96%)

Query:199 ctcctcctcctgctgctgcttctgctgc 226
|||||
Sbjct: 64 ctcctcctcctgctgctgctgctgctgc 91
CDS 4..1971

>gi|23111046|ref|NM_152227.1| Homo sapiens sorting nexin 5 (SNX5), transcript
variant 1, mRNA
Identities = 18/18 (100%)

Query: 200 tcctcctcctgctgctgc 217
|||||
Sbjct: 221 tcctcctcctgctgctgc 204
CDS 181..1395

>gi|22507392|ref|NM_022574.2| Homo sapiens PERQ amino acid rich, with GYF
domain 1 (PERQ1), mRNA
Identities = 28/31 (90%)

Query: 200 tcctcctcctgctgctgcttctgctgctcct 230
|||||
Sbjct: 1856 tcctcctcctgccgccgcttctgctcctcct 1826
CDS 236..2689

>gi|10834965|ref|NM_000404.1| Homo sapiens galactosidase, beta 1 (GLB1),
transcript variant 179423, mRNA
Identities = 26/28 (92%)

Query: 200 tcctcctcctgctgctgcttctgctgct 227
|||||
Sbjct: 83 tcctccttctgctgctggttctgctgct 110
sig_peptide 61..129
CDS 61..2094

>gi|1814019|gb|U84408.1|HSU84408 Human IL-1 receptor related protein MyD88
mRNA, complete cds
Identities = 20/20 (100%)

Query: 201 cctcctcctgctgctgcttc 220
|||||
Sbjct: 433 cctcctcctgctgctgcttc 414
CDS 61..951

>gi|15929589|gb|BC015219.1|BC015219 Homo sapiens, HBV associated factor, clone
Identities = 25/27 (92%)

Query: 201 cctcctcctgctgctgcttctgctgct 227
||||| |||||
Sbjct: 1211 cctcctgctgctgctgcttccgctgct 1185
CDS 434..1966

>gi|4885332|ref|NM_005306.1| Homo sapiens G protein-coupled receptor 43
(GPR43), mRNA
Identities = 22/23 (95%)

Query: 201 cctcctcctgctgctgcttctgc 223
||||| |||||
Sbjct: 165 cctcctcctgctgctgctgctgc 187
CDS 1..993
/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin family)"

>gi|19111149|ref|NM_133265.1| Homo sapiens angiomin (AMOT), mRNA
Identities = 24/26 (92%)

Query: 202 ctctcctgctgctgcttctgctgct 227
||||| |||||
Sbjct: 2448 ctcttctgctgctgctgctgctgct 2473
CDS 797..2824

>gi|24308357|ref|NM_033253.1| Homo sapiens 5'-nucleotidase, cytosolic IB
(NT5C1B), mRNA
Identities = 24/26 (92%)

Query: 203 tcctcctgctgctgcttctgctgctc 228
||||| |||||
Sbjct: 678 tcctcccgtgctgctgctgctgctc 653
CDS 482..1690
/note="5' nucleotidase; autoimmune infertility-related protein; 5'-nucleotidase, cytosolic IB; cytosolic 5'-nucleotidase IB; 5'-nucleotidase, cytosolic IB"

>gi|11545760|ref|NM_022055.1| Homo sapiens potassium channel, subfamily K, member 12 (KCNK12),
Identities = 22/23 (95%)

Query: 204 cctcctgctgctgcttctgctgc 226
||||| |||||
Sbjct: 59 cctcctgctgctgctgctgctgc 81
CDS 1..1293
/note="tandem pore domain potassium channel THIK-2"

>gi|5729946|ref|NM_006681.1| Homo sapiens neuromedin U (NMU), mRNA
Identities = 23/24 (95%)

Query: 205 ctctgctgctgcttctgctgctc 228
||||| |||||
Sbjct: 169 ctctgctgctgctgctgctgctc 192
CDS 106..630
sig_peptide 106..207

>gi|4128016|emb|AJ011701.1|HSA011701 Homo sapiens TRHR gene promoter and exons
1-2, partial
Identities = 20/20 (100%)

Query: 205 ctctgtgctgctgcttctgct 224
|||||
Sbjct: 1732 ctctgtgctgctgcttctgct 1751
exon 1691..1946

>gi|17985370|gb|AF284094.1|AF284094 Homo sapiens I3 binding protein (BRI3BP)
mRNA, complete cds
Identities = 22/23 (95%)

Query: 205 ctctgtgctgctgcttctgctgct 227
|||||
Sbjct: 130 ctctgtgctgctgctgctgctgct 152
CDS 88..843

>gi|15625294|gb|AF286190.1|AF286190 Homo sapiens VPS10 domain protein mRNA,
Identities = 22/23 (95%)

Query: 205 ctctgtgctgctgcttctgctgct 227
|||||
Sbjct: 5 ctctgtgctgctgctgctgctgct 27
CDS <1..>1251

>gi|28761|emb|X13629.1|HSAPOA4 Human intestinal mRNA for apolipoprotein A-IV
Identities = 22/23 (95%)

Query: 205 ctctgtgctgctgcttctgctgct 228
|||||
Sbjct: 1203 ctctgtgctgctgcttctgctgct 1181
CDS 46..1236

>gi|17458351|ref|XM_047011.2| Homo sapiens protein O-fucosyltransferase 1
(POFUT1), mRNA
Identities = 23/24 (95%)

Query: 206 tcctgtgctgctgcttctgctgctcc 229
|||||
Sbjct: 90 tcctgtgctgctgcttctgctgctcc 113.
CDS 50..1216

>gi|15812213|ref|NM_033431.1| Homo sapiens phosphodiesterase 5A, cGMP-specific
(PDE5A), transcript variant 4, mRNA
Identities = 20/20 (100%)

Query: 208 ctgctgctgcttctgctgct 227
|||||
Sbjct: 227 ctgctgctgcttctgctgct 208
CDS 156..2753

>gi|3252778|dbj|D89094.1| Homo sapiens mRNA for 3',5'-cyclic GMP
phosphodiesterase, complete
Identities = 20/20 (100%)

Query: 208 ctgctgctgcttctgctgct 227
|||||
Sbjct: 391 ctgctgctgcttctgctgct 372
CDS 320..2947

>gi|11496985|ref|NM_012072.2| Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), mRNA
Identities = 22/23 (95%)

Query: 208 ctgctgctgcttctgctgctcct 230
|||||
Sbjct: 170 ctgctgctgctgctgctgctcct 192
CDS 149..2107

>gi|4809281|ref|NM_001718.2| Homo sapiens bone morphogenetic protein 6 (BMP6),
Identities = 22/23 (95%)

Query: 208 ctgctgctgcttctgctgctcct 230
|||||
Sbjct: 533 ctgctgctgctgctgctgctcct 511
CDS 180..1721

/note="Vg-related sequence; transforming growth factor-beta"

>gi|14777259|ref|XM_027568.1| Homo sapiens similar to interleukin 9 receptor (LOC146316), mRNA
Identities = 22/23 (95%)

Query: 208 ctgctgctgcttctgctgctcct 230
|||||
Sbjct: 1294 ctgctgctgctgctgctgctcct 1272
CDS 660..1547

>gi|2626738|dbj|AB005060.1| Homo sapiens mRNA for NTAK, complete cds
Identities = 22/23 (95%)

Query: 208 ctgctgctgcttctgctgctcct 230
|||||
Sbjct: 341 ctgctgctgctgctgctgctcct 319
CDS 226..2778

>gi|4507106|ref|NM_003086.1| Homo sapiens small nuclear RNA activating complex, polypeptide 4,90kDa (SNAPC4), mRNA
Identities = 21/22 (95%)

Query: 208 ctgctgctgcttctgctgctcc 229
|||||
Sbjct: 1994 ctgctgctgctgctgctgctcc 1973

Identities = 27/29 (93%), Gaps = 1/29 (3%)

Query: 200 tcctcctc-ctgctgctgcttctgctgct 227
|||||
Sbjct: 2009 tcctcctcgtgctgctgctgctgctgct 1981
CDS 376..4785

>gi|21237798|ref|NM_139205.1| Homo sapiens histone deacetylase 5 (HDAC5), transcript variant 2,
Identities = 21/22 (95%)

Query: 208 ctgctgctgcttctgctgctcc 229
|||||
Sbjct: 1888 ctgctgctgcttctgcttctcc 1867
Identities = 15/15 (100%)

Query: 205 ctcctgctgctgctt 219
 |||||
 Sbjct: 670 ctcctgctgctgctt 656
 CDS 305..3418
 /note="isoform 2 is encoded by transcript variant 2; antigen NY-CO-9"

>gi|2564750|gb|AF029308.1|HTCRBCHR9 Homo sapiens chromosome 9 duplication of
 the T cell receptor beta locus and trypsinogen gene families
 Identities = 19/19 (100%)

Query: 209 tgctgctgcttctgctgct 227
 |||||
 Sbjct: 11391 tgctgctgcttctgctgct 11409
 V_segment join(11390..11420)

>gi|1296750|emb|Z49234.1|HSTCRB2X2 H.sapiens gene for T-cell receptor TCRBV2.2
 Identities = 19/19 (100%)

Query: 209 tgctgctgcttctgctgct 227
 |||||
 Sbjct: 976 tgctgctgcttctgctgct 994
 CDS 975..>1141

>gi|13027808|ref|NM_022718.1| Homo sapiens matrix metalloproteinase 25
 (MMP25), transcript variant 2, mRNA
 Identities = 18/18 (100%)

Query: 210 gctgctgcttctgctgct 227
 |||||
 Sbjct: 264 gctgctgcttctgctgct 281
 CDS 238..1926

>gi|12803104|gb|BC002356.1|BC002356 Homo sapiens, nucleobindin 1, clone
 Identities = 21/22 (95%)

Query: 213 gctgcttctgctgctcct 230
 |||||
 Sbjct: 68 gctgctgctgctgctcct 85

Query: 208 ctgctgctgcttctgctgctcc 229
 |||||
 Sbjct: 1235 ctgctgctgcttccgctgctcc 1214
 CDS 27..1412

>gi|24496766|ref|NM_004712.3| Homo sapiens hepatocyte growth factor-regulated
 tyrosine kinase substrate (HGS), mRNA
 Identities = 15/15 (100%)

Query: 215 tgcttctgctgctcc 229
 |||||
 Sbjct: 1732 tgcttctgctgctcc 1718
 CDS 78..2411

>gi|20544115|ref|XM_059933.5| Homo sapiens similar to putative
 lysophosphatidic acid acyltransferase (LOC137964), mRNA
 Identities = 15/15 (100%)

Query: 216 gcttctgctgctcct 230
 |||||
 Sbjct: 2233 gcttctgctgctcct 2219

CDS 913..2283

>gi|22770666|gb|AF531299.1| Homo sapiens histone H1 (HIST1H1A) gene, complete
Identities = 15/15 (100%)

Query: 216 gcttctgctgctcct 230
|||||
Sbjct: 551 gcttctgctgctcct 565
CDS 521..1168

>gi|18390058|gb|AF463518.1| Homo sapiens cell recognition protein CASPR4
(CASPR4) mRNA, complete
Identities = 15/15 (100%)

Query: 216 gcttctgctgctcct 230
|||||
Sbjct: 1568 gcttctgctgctcct 1582
CDS 140..4075
/product="cell recognition protein CASPR4"

>gi|21359973|ref|NM_053276.2| Homo sapiens vitrin (VIT), mRNA
Identities = 19/20 (95%)

Query: 216 cttctgctgctcctaccacc 236
|||||
Sbjct: 835 cttctgctgctcctaccacc 854
CDS 222..2303

>gi|23308602|ref|NM_015460.1| Homo sapiens myosin VIIA and Rab interacting
protein (MYRIP), mRNA
Identities = 15/15 (100%)

Query: 220 ctgctgctcctacca 234
|||||
Sbjct: 409 ctgctgctcctacca 423
CDS 137..2716
/product="myosin VIIA and Rab interacting protein"

>gi|15559110|gb|AF414087.1| Homo sapiens small breast epithelial mucin mRNA,
complete cds
Identities = 16/16 (100%)

Query: 220 ctgctgctcctaccac 235
|||||
Sbjct: 210 ctgctgctcctaccac 225
CDS 47..319
note="SBEM; secreted protein; similar to Mus musculus"

>gi|22779205|dbj|AB083783.1| Homo sapiens slac2-c mRNA for Slp homologue
lacking C2 domains-c, complete cds
Identities = 15/15 (100%)

Query: 220 ctgctgctcctacca 234
|||||
Sbjct: 273 ctgctgctcctacca 287
CDS 1..2580

>gi|7705267|ref|NM_016255.1| Homo sapiens family with sequence similarity 8,
member A1 (FAM8A1),
Identities = 15/15 (100%)

Query: 226 ctcctaccaccgccg 240
 |||||
 Sbjct: 147 ctcctaccaccgccg 161
 CDS 56..1297
 /product="Autosomal Highly Conserved Protein"

>gi|14210509|ref|NM_032496.1| Homo sapiens rho-gtpase activating protein
 ARHGAP9 (ARHGAP9), mRNA
 Identities = 15/15 (100%)

Query: 240 gcctctggtgccacc 254
 |||||
 Sbjct: 2335 gcctctggtgccacc 2349
 CDS 407..2659
 /product="hypothetical protein MGC12959"

>gi|184756|gb|J00221.1|HUMIGCD7 Human Ig germline H-chain G-E-A region B:
 alpha-2 A2m(1) allele constant region, 3' end
 Identities = 15/15 (100%)

Query: 240 gcctctggtgccacc 254
 |||||
 Sbjct: 800 gcctctggtgccacc 814
 CDS join(<164..469,684..1004,1227..1621)
 /product="immunoglobulin alpha-2 heavy chain"

>gi|21361375|ref|NM_007165.2| Homo sapiens splicing factor 3a, subunit 2,
 66kDa (SF3A2), mRNA
 Identities = 16/16 (100%)

Query: 248 tgccaccgcccccgcc 263
 |||||
 Sbjct: 876 tgccaccgcccccgcc 891
 CDS 125..1519
 /note="Spliceosome protein SAP-62; splicing factor 3a,
 subunit 2, 66kD"

>gi|21361291|ref|NM_005611.2| Homo sapiens retinoblastoma-like 2 (p130)
 (RBL2), mRNA
 Identities = 15/15 (100%)

Query: 249 gccaccgcccccgcc 263
 |||||
 Sbjct: 93 gccaccgcccccgcc 107
 CDS 70..3489

>gi|4505322|ref|NM_003941.1| Homo sapiens Wiskott-Aldrich syndrome-like
 (WASL), mRNA
 Identities = 15/15 (100%)

Query: 249 gccaccgcccccgcc 263
 |||||
 Sbjct: 1406 gccaccgcccccgcc 1420
 CDS 255..1772

>gi|5901937|ref|NM_007021.1| Homo sapiens decidual protein induced by
 progesterone (DEPP), mRNA
 Identities = 15/15 (100%)

Query: 249 gccaccgcccccgcc 263
|||||
Sbjct: 787 gccaccgcccccgcc 801
CDS 219..857

>gi|22045278|ref|XM_001334.5| Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1),
Identities = 16/16 (100%)

Query: 250 ccaccgcccccgccg 265
|||||
Sbjct: 1326 ccaccgcccccgccg 1341
CDS 36..1391

/product="similar to Octamer-binding transcription factor 6 (OCT-6) (POU-domain transcription factor SCIP) (TST-1)"

>gi|24234749|ref|NM_012218.2| Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 1, mRNA
Identities = 15/15 (100%)

Query: 250 ccaccgcccccgccg 264
|||||
Sbjct: 2389 ccaccgcccccgccg 2375
CDS 267..2951

/note="isoform a is encoded by transcript variant 1; double-stranded RNA-binding protein, 76 kD; M-phase phosphoprotein 4; nuclear factor associated with dsRNA; nuclear factor of activated T-cells, 90 kD; translational control protein 80"

>gi|190749|gb|M96684.1|HUMPURA H.sapiens Pur (pur-alpha) mRNA, complete cds
Identities = 16/16 (100%)

Query: 250 ccaccgcccccgccg 265
|||||
Sbjct: 163 ccaccgcccccgccg 148
CDS 60..1028

/function="sequence-specific single-stranded DNA binding protein"

>gi|4885128|ref|NM_005194.1| Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB),
Identities = 15/15 (100%)

Query: 250 ccaccgcccccgccg 264
|||||
Sbjct: 484 ccaccgcccccgccg 498
CDS 1..1038

>gi|24850134|ref|NM_170695.1| Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF),
Identities = 18/19 (94%)

Query: 253 ccgcccccgccggtgccg 271
|||||
Sbjct: 374 ccgcccccgccgagccg 356
CDS 304..1509

>gi|20805946|gb|AY083269.1| Homo sapiens transcription factor mammalian MafA gene, complete cds
Identities = 18/19 (94%)

Query: 253 ccgccccgcggtgcccg 271
 ||||| |||||
 Sbjct: 236 ccgccccgcggtgcccg 218
 CDS 1..1059

>gi|5058992|gb|U66095.1|U66095 Homo sapiens cell-line THP-1 GTP cyclohydrolase I mRNA, complete
 Identities = 15/15 (100%)

Query: 257 ccccgccggtgcccg 271
 |||||
 Sbjct: 177 ccccgccggtgcccg 163
 CDS 145..846

>gi|4507750|ref|NM_001071.1| Homo sapiens thymidylate synthetase (TYMS), mRNA
 Identities = 15/15 (100%)

Query: 261 gccggtgcccggtgcg 275
 |||||
 Sbjct: 267 gccggtgcccggtgcg 253
 CDS 106..1047

>gi|17511946|gb|BC018929.1|BC018929 Homo sapiens, Similar to T-cell death associated gene, clone
 Identities = 15/15 (100%)

Query: 261 gccggtgcccggtgcg 275
 |||||
 Sbjct: 1029 gccggtgcccggtgcg 1015
 CDS 279..1058

>gi|6679302|ref|NM_007350.1| Homo sapiens pleckstrin homology-like domain, family A, member 1 (PHLDA1), mRNA
 Identities = 15/15 (100%)

Query: 261 gccggtgcccggtgcg 275
 |||||
 Sbjct: 1333 gccggtgcccggtgcg 1319
 CDS 160..1362

>gi|23097243|ref|NM_152891.1| Homo sapiens serine protease EOS (EOS), mRNA
 Identities = 19/20 (95%)

Query: 263 cggtgcccggtgcgaccggtg 282
 |||||
 Sbjct: 385 cggtgcccggtgcgaccggtg 404
 CDS 69..923

>gi|20555609|ref|XM_165720.1| Homo sapiens HCR (a-helix coiled-coil rod homologue) (HCR), mRNA
 Identities = 15/15 (100%)

Query: 275 gaccggtggtggtag 289
 |||||
 Sbjct: 1573 gaccggtggtggtag 1559
 CDS 80..2428

>gi|10947055|ref|NM_020987.1| Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
 Identities = 21/21 (100%)

Query: 280 gtggtggttagtggtggtggtg 300
 |||||
Sbjct: 12113 gtggtggttagtggtggtggtg 12093

Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
 |||||
Sbjct: 12096 ggtggtggcagtggtggtggtg 12075

Identities = 18/18 (100%)

Query: 279 ggtggtggttagtggtggt 296
 |||||
Sbjct: 12123 ggtggtggttagtggtggt 12106

Identities = 20/22 (90%)

Query: 279 ggtggtggttagtggtggtggtg 300
 |||||
Sbjct: 12111 ggtggttagtggtggtggtggtg 12090

Identities = 19/21 (90%)

Query: 279 ggtggtggttagtggtggtggt 299
 |||||
Sbjct: 12126 ggtggtggtggttagtggtggt 12106

Identities = 13/13 (100%)

Query: 279 ggtggtggttagtg 291
 |||||
Sbjct: 12081 ggtggtggttagtg 12069
CDS 193..13326

>gi|7662227|ref|NM_014841.1| Homo sapiens synaptosomal-associated protein,
91kDa homolog (mouse) (SNAP91), mRNA
Identities = 20/20 (100%)

Query: 279 ggtggtggttagtggtggtgg 298
 |||||
Sbjct: 1890 ggtggtggttagtggtggtgg 1871
CDS 244..2967

Identities = 14/14 (100%)

Query: 279 ggtggtggttagtggtggtgg 292
 |||||
Sbjct: 717 ggtggtggttagtggtggtgg 704

Identities = 19/21 (90%)

Query: 279 ggtggtggttagtggtggtggt 299
 |||||
Sbjct: 729 ggtggttagtggtggtggtggt 709
CDS 320..1168

>gi|5453935|ref|NM_006236.1| Homo sapiens POU domain, class 3, transcription factor 3 (POU3F3),
Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
||||||| |||||
Sbjct: 829 ggtggtggtggtggtggtggtg 808
CDS 1..1503

>gi|21396478|ref|NM_005924.2| Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA
Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
||||||| |||||
Sbjct: 404 ggtggtggtggtggtggtggtg 383

Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
||||||| |||||
Sbjct: 407 ggtggtggtggtggtggtggtg 386

Identities = 20/22 (90%)

Query: 279 ggtggtggttagtggtggtggtg 300
|||||| | |||||
Sbjct: 416 ggtggtgatggtggtggtggtg 395
CDS 182..1093

>gi|21361336|ref|NM_001969.2| Homo sapiens eukaryotic translation initiation factor 5 (EIF5), mRNA
Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
||||||| |||||
Sbjct: 1022 ggtggtggtggtggtggtggtg 1001

Identities = 19/20 (95%)

Query: 281 tggtagtggtggtggtggtg 300
||||||| |||||
Sbjct: 1023 tggtagtggtggtggtggtg 1004
CDS 469..1764

>gi|12597624|ref|NM_012068.2| Homo sapiens activating transcription factor 5 (ATF5), mRNA
Identities = 20/20 (100%)

Query: 281 tggtagtggtggtggtggtg 300
|||||||
Sbjct: 730 tggtagtggtggtggtggtg 711

>gi|20127494|ref|NM_006237.2| Homo sapiens POU domain, class 4, transcription factor 1 (POU4F1),
Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300
||||||| |||||
Sbjct: 553 ggtggtggtggtggtggtggtg 532

Identities = 21/22 (95%)

Query: 279 ggtggtggttagtggtggtggtg 300

||||||| |||||||||

Sbjct: 556 ggtggtggtggtggtggtggtg 535

Identities = 19/20 (95%)

Query: 281 tggtagtggtggtggtggtg 300

||||||| |||||||||

Sbjct: 560 tggtagtggtggtggtggtg 541

CDS 235..1497

>gi|20379115|gb|AF498971.1| Homo sapiens small GTP binding protein RhoB (ARHB) mRNA, complete

Identities = 15/15 (100%)

Query:299 tggtagtggtgggcg 313

|||||||

Sbjct: 23 tggtagtggtgggcg 37

CDS 1..591

>gi|190939|gb|M38453.1|HUMRASTG Human ras transforming protein gene, exon 1

Identities = 15/15 (100%)

Query: 299 tggtagtggtgggcg 313

|||||||

Sbjct: 149 tggtagtggtgggcg 163

exon 133..243

>gi|20544140|ref|NM_003185.2| Homo sapiens TAF4 RNA polymerase II, TATA box binding protein(TBP)-associated factor, 135kDa (TAF4), mRNA

Identities = 14/14 (100%)

Query: 299 tggtagtggtgggc 312

|||||||

Sbjct: 125 tggtagtggtgggc 112

CDS 1..3252

>gi|21361862|ref|NM_033104.2| Homo sapiens stonin 2 (STN2), mRNA

Identities = 14/14 (100%)

Query: 299 tggtagtggtgggc 312

|||||||

Sbjct: 2110 tggtagtggtgggc 2097

CDS 202..2919

>gi|22597105|gb|AF521671.1| Homo sapiens SWI/SNF chromatin remodeling complex subunit OSA2

Identities = 14/14 (100%)

Query:299 tggtagtggtgggc 312

|||||||

Sbjct: 68 tggtagtggtgggc 55

CDS <1..6498

>gi|22051956|ref|XM_113625.2| Homo sapiens similar to Antrax toxin receptor precursor (Tumor endothelial marker 8) (LOC195977), mRNA

Identities = 14/14 (100%)

Query: 299 tggtagtggtgggc 312

|||||||

Sbjct: 411 tggtagtggtgggc 398

CDS 251..1171

>gi|17863992|gb|AF449430.1|AF449430 Homo sapiens endocytosis protein HSTNB
variant mRNA, complete cds
Identities = 14/14 (100%)

Query: 299 tgggtggtggtgggc 312
|||||
Sbjct: 2110 tgggtggtggtgggc 2097
CDS 202..2919

>gi|11065969|gb|AF193855.1|AF193855 Homo sapiens zinc finger protein of
cerebellum ZIC2 (ZIC2) mRNA,
Identities = 14/14 (100%)

Query: 299 tgggtggtggtgggc 312
|||||
Sbjct: 701 tgggtggtggtgggc 688
CDS 1..1599

>gi|17474021|ref|XM_058523.1| Homo sapiens similar to MDM2 variant FB29
(LOC121015), mRNA
Identities = 14/14 (100%)

Query: 302 tgggtggtgggcggg 315
|||||
Sbjct: 117 tgggtggtgggcggg 104
CDS 26..418

>gi|21361620|ref|NM_002633.2| Homo sapiens phosphoglucomutase 1 (PGM1), mRNA
Identities = 14/14 (100%)

Query: 302 tgggtggtgggcggg 315
|||||
Sbjct: 383 tgggtggtgggcggg 396
CDS 214..1902

>gi|6979929|gb|AF221759.1|AF221759 Homo sapiens Mam1 mRNA, partial cds
Identities = 14/14 (100%)

Query: 303 ggtggtgggcgggt 316
|||||
Sbjct: 1643 ggtggtgggcgggt 1630
CDS <1..2682

>gi|4505736|ref|NM_002621.1| Homo sapiens properdin P factor, complement
(PFC), mRNA
Identities = 14/14 (100%)

Query: 306 ggtgggcgggtact 320
|||||
Sbjct: 1493 ggtgggcgggtact 1480
CDS 243..1652

>gi|20127484|ref|NM_005654.2| Homo sapiens nuclear receptor subfamily 2, group
F, member 1 (NR2F1), mRNA
Identities = 14/14 (100%)

Query: 319 tagcgcgacgtggg 332
|||||
Sbjct: 705 tagcgcgacgtggg 692
CDS 98..1369

/note="Transcription factor COUP 1 (chicken ovalbumin upstream promoter 1,;
transcription factor COUP 1 "

>gi|16418382|ref|NM_052876.1| Homo sapiens transcriptional repressor NAC1
(NAC1), mRNA
Identities = 15/15 (100%)

Query: 326 acgtgggcgaccagt 340
|||||
Sbjct: 404 acgtgggcgaccagt 418
CDS 127..1710
/note="contains POZ domain"

>gi|16445431|ref|NM_033662.1| Homo sapiens WD repeat domain 4 (WDR4),
transcript variant 3, mRNA
Identities = 16/16 (100%)

Query: 328 gtgggcgaccagtggc 343
|||||
Sbjct: 882 gtgggcgaccagtggc 897
CDS 363..1163
/note="isoform 2 is encoded by transcript variant 3; WD repeat-containing
protein 4"

>gi|22027497|ref|NM_012295.2| Homo sapiens calcineurin binding protein 1
(CABIN1), mRNA
Identities = 15/15 (100%)

Query: 334 gaccagtggctgctg 348
|||||
Sbjct: 1787 gaccagtggctgctg 1801
CDS 128..6790

>gi|20336259|ref|NM_015866.2| Homo sapiens PR domain containing 2, with ZNF
domain (PRDM2), transcript variant 2, mRNA
Identities = 14/14 (100%)

Query: 336 ccagtggctgctgg 349
|||||
Sbjct: 3329 ccagtggctgctgg 3316
CDS 857..5905
/note="isoform b is encoded by transcript variant 2; zinc-finger DNA-binding
protein; retinoblastoma protein-interacting zinc finger protein; MTE-binding
protein"

>gi|22042322|ref|XM_015428.3| Homo sapiens similar to CGI-105 protein
(LOC151313), mRNA
Identities = 14/14 (100%)

Query: 337 cagtggctgctggg 350
|||||
Sbjct: 620 cagtggctgctggg 633
CDS 11..955

>gi|20270612|ref|NG_001318.1| Homo sapiens HSP40 pseudogene (HSP40)
Identities = 14/14 (100%)

Query: 337 cagtggctgctggg 350
|||||
Sbjct: 2499 cagtggctgctggg 2486
misc_feature 1..2882

>gi|21265045|ref|NM_139027.1| Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 13 (ADAMTS13), transcript variant 2, mRNA
Identities = 17/17 (100%)

Query: 339 gtggctgctgggctggg 355
 |||||
Sbjct: 3812 gtggctgctgggctggg 3828
 CDS 445..4560
(vWF)-cleaving protease, which is responsible for cleaving at the

>gi|22050832|ref|XM_114863.2| Homo sapiens similar to alpha 2 type IV collagen preproprotein; canstatin (LOC203630), mRNA
Identities = 16/16 (100%)

Query: 339 gtggctgctgggctggg 354
 |||||
Sbjct: 450 gtggctgctgggctggg 465
 CDS 1..1425
/product="similar to alpha 2 type IV collagen preproprotein; canstatin"

>gi|22064435|ref|XM_017037.3| Homo sapiens suppressor of Ty 6 homolog (S. cerevisiae) (SUPT6H),
Identities = 15/15 (100%)

Query: 340 tggctgctgggctggg 354
 |||||
Sbjct: 4624 tggctgctgggctggg 4610
 CDS 161..4972

>gi|20149786|gb|AF039196.3| Homo sapiens putative single zinc finger transcription factor protein (hairless) mRNA, complete cds
Identities = 15/15 (100%)

Query: 341 ggctgctgggctggg 355
 |||||
Sbjct: 4218 ggctgctgggctggg 4204
 CDS 1485..5054
/note="restricted expression in the brain and skin"

>gi|20070162|ref|NM_018896.2| Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
Identities = 15/15 (100%)

Query: 342 gctgctgggctgggt 356
 |||||
Sbjct: 1440 gctgctgggctgggt 1426
 CDS 1..7134

>gi|18564486|ref|XM_094865.1| Homo sapiens similar to Olfactory receptor 4F3 (LOC168119), mRNA
Identities = 15/15 (100%)

Query: 343 ctgctgggctgggtt 357
 |||||
Sbjct: 49 ctgctgggctgggtt 35
 CDS 1..978

>gi|4503532|ref|NM_001417.1| Homo sapiens eukaryotic translation initiation factor 4B (EIF4B),

Identities = 16/16 (100%)

Query: 350 gctgggttcacgtggt 365
 |||||
Sbjct: 393 gctgggttcacgtggt 378
 CDS 1..1836

>gi|4557252|ref|NM_001109.1| Homo sapiens a disintegrin and metalloproteinase domain 8 (ADAM8),
Identities = 15/15 (100%)

Query: 360 cgtggtggtggttct 374
 |||||
Sbjct: 1980 cgtggtggtggttct 1994
 CDS 10..2484

>gi|20143921|ref|NM_133437.1| Homo sapiens titin (TTN), transcript variant novex-2, mRNA
Identities = 17/18 (94%)

Query: 360 cgtggtggtggttctcca 377
 |||| |
Sbjct: 33611 cgtgatggtggttctcca 33628
 CDS 224..81580
/note="isoform novex-2 is encoded by transcript variant novex-2; connectin; CMH9, included"

>gi|22726242|gb|BC037404.1| Homo sapiens, Similar to formin binding protein 4, clone MGC:36749
Identities = 14/14 (100%)

Query: 361 gtggtggtggttct 374
 |||||
Sbjct: 2743 gtggtggtggttct 2730
 CDS 28..3075

>gi|4557234|ref|NM_000018.1| Homo sapiens acyl-Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene encoding mitochondrial protein, mRNA
Identities = 14/14 (100%)

Query: 362 tgggtggtggttctc 375
 |||||
Sbjct: 1818 tgggtggtggttctc 1831
 CDS 86..2053

>gi|22048275|ref|XM_063346.3| Homo sapiens similar to polypyrimidine-tract binding protein(LOC122888), mRNA
Identities = 14/14 (100%)

Query: 363 ggtggtggttctcc 376
 |||||
Sbjct: 1345 ggtggtggttctcc 1332
 CDS 1..1461

>gi|4885524|ref|NM_005490.1| Homo sapiens SH2 domain containing 3A (SH2D3A),
Identities = 15/15 (100%)

Query: 390 ctgcgcgctcctcca 414
 |||||
Sbjct: 1319 ctgcgcgctcctcca 1305
 CDS 152..1882

>gi|22060841|ref|XM_165659.2| Homo sapiens elaC homolog 1 (E. coli) (ELAC1), mRNA
Identities = 16/16 (100%)

Query: 397 ctctccatcacccac 412
 |||||
Sbjct: 894 ctctccatcacccac 879
 CDS 108..1199
/product="similar to elaC homolog 1 (E. coli); similar to Escherichia coli elaC;
hypothetical protein D29; elaC

>gi|9055315|ref|NM_012406.2| Homo sapiens PR domain containing 4 (PRDM4), mRNA
Identities = 15/15 (100%)

Query: 397 ctctccatcaccca 411
 |||||
Sbjct: 1109 ctctccatcaccca 1123
 CDS 123..2528

>gi|22046620|ref|XM_069728.3| Homo sapiens similar to beta-glucuronidase (LOC136132), mRNA
Identities = 15/15 (100%)

Query: 399 tctccatcacccac 413
 |||||
Sbjct: 663 tctccatcacccac 649
 CDS 1..972

>gi|19263734|gb|BC025358.1| Homo sapiens, ATP-binding cassette, sub-family D (ALD), member 1,
Identities = 15/15 (100%)

Query: 400 ctccatcacccaccg 414
 |||||
Sbjct: 2364 ctccatcacccaccg 2378
 CDS 400..2637

>gi|11968022|ref|NM_022473.1| Homo sapiens zinc finger protein 106 (ZFP106), mRNA
Identities = 15/15 (100%)

Query: 400 ctccatcacccaccg 414
 |||||
Sbjct: 3838 ctccatcacccaccg 3852
 CDS 336..5987

>gi|18586624|ref|XM_085530.1| Homo sapiens similar to Adrenoleukodystrophy protein (ALDP)
Identities = 15/15 (100%)

Query: 400 ctccatcacccaccg 414
 |||||
Sbjct: 310 ctccatcacccaccg 324
 CDS 134..583
 misc_feature 161..376

>gi|19743876|ref|NM_002918.2| Homo sapiens regulatory factor X, 1 (influences HLA class II expression) (RFX1), mRNA

Identities = 15/15 (100%)

Query: 406 caccacccgctgctg 420

|||||

Sbjct: 220 caccacccgctgctg 234

CDS 93..3032

>gi|19263734|gb|BC025358.1| Homo sapiens, ATP-binding cassette, sub-family D (ALD), member 1,

Identities = 15/15 (100%)

Query: 410 ctccatcacccaccg 424

|||||

Sbjct: 2364 ctccatcacccaccg 2378

CDS 400..2637

>gi|18586624|ref|XM_085530.1| Homo sapiens similar to Adrenoleukodystrophy protein (ALDP) (LOC146640), mRNA

Identities = 15/15 (100%)

Query: 410 ctccatcacccaccg 424

|||||

Sbjct: 310 ctccatcacccaccg 324

CDS 134..583

>gi|11968022|ref|NM_022473.1| Homo sapiens zinc finger protein 106 (ZFP106), mRNA

Identities = 15/15 (100%)

Query: 410 ctccatcacccaccg 424

|||||

Sbjct: 3838 ctccatcacccaccg 3852

CDS 336..5987

>gi|13184045|ref|NM_023944.1| Homo sapiens cytochrome P450, subfamily IVF, polypeptide 12 (CYP4F12), mRNA

Identities = 17/17 (100%)

Query: 413 cgctgctgagcctgccc 429

|||||

Sbjct: 35 cgctgctgagcctgccc 51

CDS 31..1605

>gi|23821028|ref|NM_153486.1| Homo sapiens lactate dehydrogenase D (LDHD), mRNA

Identities = 20/22 (90%)

Query: 424 ctgcccgcgcgcggctcctgc 445

|||||

Sbjct: 637 ctgcccgcgcggcggtgctgc 658

CDS 58..1518

>gi|24528580|gb|AF079529.2| Homo sapiens cAMP-specific phosphodiesterase 8B1 (PDE8B) mRNA, complete cds; alternatively spliced

Identities = 15/15 (100%)

Query: 427 cccgacgcgcggctc 441

|||||

Sbjct: 224 cccgacgcgcggctc 210

CDS 46..2703

>gi|22001416|ref|NM_015465.1| Homo sapiens gemin 5 (GEMIN5), mRNA
SMN complex component; Sm-interacting protein; DKFZP586M1824 protein
Identities = 14/14 (100%)

Query:434 cgcggtcctgcc 447
|||||
Sbjct: 17 cgcggtcctgcc 4
CDS 1..4527

>gi|29459|emb|X68149.1|HSBLR1A Homo sapiens BLR1 gene for Burkitt's lymphoma
receptor 1
Identities = 18/19 (94%)

Query: 434 cgcggtcctgcccaagct 452
|||||
Sbjct: 1085 cgcggtcctgcccaagct 1103
CDS 85..1203

>gi|840783|emb|X68829.1|HSMDCR H.sapiens mRNA for MDR15 protein
Identities = 18/19 (94%)

Query: 434 cgcggtcctgcccaagct 452
|||||
Sbjct: 1154 cgcggtcctgcccaagct 1172
CDS 289..1272

>gi|5032094|ref|NM_005630.1| Homo sapiens solute carrier family 21
(prostaglandin transporter), member 2 (SLC21A2), mRNA
Identities = 17/17 (100%)

Query: 437 ggctcctgcccaagctc 453
|||||
Sbjct: 88 ggctcctgcccaagctc 104
CDS 84..2015

>gi|4505876|ref|NM_000445.1| Homo sapiens plectin 1, intermediate filament
binding protein 500kDa (PLEC1), mRNA
Identities = 17/18 (94%)

Query: 438 gctcctgcccaagctcct 455
|||||
Sbjct: 7156 gctcctgcgcaagctcct 7139
CDS 52..13776

/function="high molecular weight cytoskeletal-associated protein which is a
component of hemidesmosomes in basal keratinocytes and also a component of the
sarcolemma in muscle (HD1)

>gi|22058106|ref|XM_171754.1| Homo sapiens similar to a disintegrin-like and
metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17
preproprotein (LOC257018), mRNA
Identities = 15/15 (100%)

Query: 438 gctcctgcccaagct 452
|||||
Sbjct: 91 gctcctgcccaagct 77
CDS 1..420

>gi|4505936|ref|NM_002693.1| Homo sapiens polymerase (DNA directed), gamma
(POLG), nuclear gene encoding mitochondrial protein, mRNA
Identities = 14/14 (100%)

Query: 438 gctcctgccaagc 451
 |||
 Sbjct: 1953 gctcctgccaagc 1966
 CDS 283..4002

>gi|533527|gb|U10694.1|HSU10694 Human MAGE-9 antigen (MAGE9) gene, complete cds
 Identities = 18/19 (94%)

Query: 438 gctcctgccaagctcctg 456
 |||
 Sbjct: 1290 gctcctgcccacgctcctg 1308
 exon 1268..>2845
 CDS 1333..2280

>gi|4758361|ref|NM_004112.1| Homo sapiens fibroblast growth factor 11 (FGF11), mRNA
 Identities = 16/16 (100%)

Query: 442 ctgccaagctcctgg 457
 |||
 Sbjct: 589 ctgccaagctcctgg 604
 CDS 1..678

>gi|13435128|ref|NM_022089.1| Homo sapiens putative ATPase (HSA9947), mRNA
 Identities = 17/18 (94%)

Query: 442 ctgccaagctcctggtc 459
 |||
 Sbjct: 2555 ctgccaagctcctggtc 2572
 CDS 35..3577

>gi|24308028|ref|NM_015296.1| Homo sapiens zizimin1 (zizimin1), mRNA
 Identities = 14/14 (100%)

Query: 445 cccaagctcctgggt 458
 |||
 Sbjct: 2431 cccaagctcctgggt 2418
 CDS 56..6265
 note="Cdc42 activator"

>gi|22043940|ref|XM_060678.5| Homo sapiens similar to Synaptotagmin II (SytII) (LOC127833), mRNA
 Identities = 14/14 (100%)

Query: 445 cccaagctcctgggt 458
 |||
 Sbjct: 540 cccaagctcctgggt 527
 CDS 1..1278

>gi|18599586|ref|XM_092362.1| Homo sapiens similar to evidence:NAS~hypothetical protein~putative (LOC165086), mRNA
 Identities = 17/18 (94%)

Query: 448 aagctcctggtctaggag 465
 |||
 Sbjct: 776 aagctcctggtctgggag 759
 CDS 1..936

>gi|23336903|tpg|BK000566.1| TPA: Homo sapiens SF3b125 DEAD-box protein mRNA, complete cds,

Identities = 14/14 (100%)

Query: 452 tcctggtctaggag 465
|||||||
Sbjct: 399 tcctggtctaggag 386
CDS 1..2460

>gi|22052707|ref|XM_172523.1| Homo sapiens similar to N-formyl peptide
receptor (LOC256135), mRNA
Identities = 14/14 (100%)

Query: 460 taggagtaaggcca 473
|||||||
Sbjct: 410 taggagtaaggcca 397
CDS 81..560

>gi|474428|emb|Z31702.1|HSP53DN H.sapiens p5-3 DNA
Identities = 16/16 (100%)

Query: 461 aggagtaaggccatgg 476
|||||||
Sbjct: 264 aggagtaaggccatgg 279
1..1464

Non-homologous recombination within the major histocompatibility
complex creates a transcribed hybrid sequence

>gi|18550199|ref|XM_059368.2| Homo sapiens similar to thymidylate kinase
family LPS-inducible member; thymidylate kinase homologue (LOC129607), mRNA
Identities = 14/14 (100%)

Query: 467 aaggccatgggcg 480
|||||||
Sbjct: 23 aaggccatgggcg 10
CDS 16..1365

>gi|6706902|emb|AL109827.8|HSJ309K20 Human DNA sequence from clone RP1-309K20
on chromosome 20 Contains the gene for a novel protein similar to dysferlin, the
SPAG4 gene for sperm associated antigen 4, the CPNE1 gene for Copine I (similar
to KIAA0636), the gene KIAA0765 (HRIHFB2091) for an RNA recognition motif
(RNP, RRM or RBD domain) containing protein and the 3' end of the NIFS
gene for cysteine desulfurase.
Identities = 16/16 (100%)

Query: 468 aggccatgggcgcg 483
|||||||
Sbjct: 7506 aggccatgggcgcg 7491
CDS 7357..7540

>gi|21614532|ref|NM_144957.1| Homo sapiens protease, serine, 21 (testisin)
(PRSS21), transcript variant 3, mRNA
Identities = 14/14 (100%)

Query: 468 aggccatgggcgcg 481
|||||||
Sbjct: 102 aggccatgggcgcg 115
CDS 107..1009

>gi|18087852|ref|NM_080672.1| Homo sapiens Q9H4T4 like (H17739), mRNA
Identities = 18/19 (94%)

Query: 469 ggccatgggcgcggccggc 487
 |||||
 Sbjct: 141 ggccatgggccggccggc 123
 CDS 136..1815

>gi|790818|gb|L39891.1|HUMPKD1GEN Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, Identities = 16/16 (100%)

Query: 475 gggcgcgccggccgc 490
 |||||
 Sbjct: 50097 gggcgcgccggccgc 50082
 CDS 49997..50171

>gi|24429581|ref|NM_153813.1| Homo sapiens friend of GATA-1 (FOG1), mRNA Identities = 14/14 (100%)

Query: 475 gggcgcgccggcc 487
 |||||
 Sbjct: 2503 gggcgcgccggcc 2490
 CDS 323..3337

>gi|22094134|ref|NM_032482.1| Homo sapiens histone methyltransferase DOT1L (DOT1L), mRNA Identities = 14/14 (100%)

Query: 476 ggcgcggccggccg 489
 |||||
 Sbjct: 2314 ggcgcggccggccg 2301
 CDS 37..4650
 function="methylates lysine 79 of histone H3"

>gi|4759111|ref|NM_004207.1| Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3), mRNA Identities = 14/14 (100%)

Query: 477 gcgcggccggccgc 490
 |||||
 Sbjct: 891 gcgcggccggccgc 904
 CDS 63..1460

>gi|20544351|ref|XM_005702.8| Homo sapiens wingless-type MMTV integration site family, member 8B (WNT8B), mRNA Identities = 14/14 (100%)

Query: 477 gcgcggccggccgc 490
 |||||
 Sbjct: 808 gcgcggccggccgc 821
 CDS 129..1184

>gi|23452045|gb|AF494409.1| Homo sapiens pantothenate kinase 2 mRNA, complete cds Identities = 15/15 (100%)

Query: 480 cggccggccgcctct 494
 |||||
 Sbjct: 279 cggccggccgcctct 265
 CDS 7..1719

gi|2213644|gb|U63833.1|HSU63833 Human PAX6 gene, promoter region and exons 1 and 2

Identities = 16/16 (100%)

Query: 482 gccggccgcctctgct 497

|||||

Sbjct: 114 gccggccgcctctgct 129

promoter 1..3274

/note="isoform 2 is encoded by transcript variant 2; ortholog of mouse CNR5; KIAA0345-like 1"

>gi|14589892|ref|NM_001794.2| Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA

Identities = 15/15 (100%)

Query: 483 ccggccgcctctgct 497

|||||

Sbjct: 2841 ccggccgcctctgct 2827

CDS 15..2765

This gene is a classical cadherin from the cadherin superfamily. The encoded protein is a calcium-dependent cell-cell adhesion glycoprotein. studies

>gi|11545830|ref|NM_022114.1| Homo sapiens PR domain containing 16 (PRDM16), mRNA/ Identities = 15/15 (100%)

Query: 483 ccggccgcctctgct 497

|||||

Sbjct: 1638 ccggccgcctctgct 1652

gene 1..4376

>gi|14165396|ref|NM_031865.1| Homo sapiens protocadherin alpha 13 (PCDHA13), transcript variant 2,

Identities = 16/16 (100%)

Query: 484 cggccgcctctgctgc 499

|||||

Sbjct: 2268 cggccgcctctgctgc 2253

CDS 1..2424

>gi|12697311|emb|AJ295990.1|HSA295990 Homo sapiens mRNA for putative chromatin modulator, alternative splice NSD3L

Identities = 15/15 (100%)

Query: 485 ggccgcctctgctgc 499

|||||

Sbjct: 4514 ggccgcctctgctgc 4528

CDS 314..4627

/note="alternative splice NSD3L"

<gi|12642816|gb|AF332469.1|AF332469 Homo sapiens putative protein WHSC1L11 (WHSC1L1) mRNA, complete cds, alternatively spliced

Identities = 15/15 (100%)

Query: 485 ggccgcctctgctgc 499

|||||

Sbjct: 4719 ggccgcctctgctgc 4733

CDS 519..4832

>gi|17474463|ref|XM_062506.1| Homo sapiens similar to 60S acidic ribosomal protein P2(LOC121193), mRNA

Identities = 15/15 (100%)

Query: 485 ggccgcctctgctgc 499
 |||||
 Sbjct: 278 ggccgcctctgctgc 292
 CDS 1..351
 product="similar to 60S acidic ribosomal protein P2"
 >gi|22035673|ref|NM_006031.2| Homo sapiens pericentrin 2 (kendrin) (PCNT2), mRNA
 Score = 30.2 bits (15), Expect = 88
 Identities = 15/15 (100%)

Query: 487 ccgcctctgctgcag 501
 |||||
 Sbjct: 3442 ccgcctctgctgcag 3428
 CDS 53..10063
 The protein encoded by this gene binds to calmodulin and is expressed in the centrosome.

>gi|12620204|gb|AF288398.1|AF288398 Homo sapiens Clorf14 mRNA, complete cds
 Identities = 16/16 (100%)

Query: 489 gcctctgctgcagatg 504
 |||||
 Sbjct: 1282 gcctctgctgcagatg 1267
 CDS 69..2246
 note="alternatively spliced"

>gi|9622520|gb|AF173157.1|AF173157 Homo sapiens MSTP098 (MST098) mRNA, complete cds
 Identities = 16/16 (100%)

Query: 489 gcctctgctgcagatg 504
 |||||
 Sbjct: 329 gcctctgctgcagatg 314
 CDS 239..460

>gi|22046810|ref|XM_089096.2| Homo sapiens similar to coxsackievirus and adenovirus receptor-like protein (LOC163724), mRNA
 Identities = 15/15 (100%)

Query: 490 cctctgctgcagatg 504
 |||||
 Sbjct: 578 cctctgctgcagatg 564
 CDS 291..1466
 misc_feature 552..674

>gi|20070194|ref|NM_006140.2| Homo sapiens colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) (CSF2RA), mRNA
 Identities = 17/18 (94%)

Query: 512 tctgcgaccagtggcacc 529
 ||||| |||||
 Sbjct: 248 tctgcgaccagtggcacc 265
 CDS 171..1373
 >gi|15990415|gb|BC015569.1|BC015569 Homo sapiens, Similar to SRp25 nuclear protein,
 Identities = 14/14 (100%)

Query: 517 gaccagtggcaccg 430
 |||||
 Sbjct: 406 gaccagtggcaccg 419
 CDS 37..684

>gi|13624213|gb|AF319045.1|AF319045 Homo sapiens contactin-associated protein
2 (CNTNAP2) mRNA, complete
Identities = 14/14 (100%)

Query: 517 gaccagtggcaccg 530
|||||
Sbjct: 2778 gaccagtggcaccg 2791
CDS 141..4136

>gi|14702161|ref|NM_032421.1| Homo sapiens cytoplasmic linker 2 (CYLN2),
transcript variant 2,
Identities = 14/14 (100%)

Query: 519 ccagtggcaccgcc 532
|||||
Sbjct: 314 ccagtggcaccgcc 327
CDS 328..3363
note="synonyms: WSCR4, WBSCR4, CLIP-115, KIAA0291, MGC11333"
note="isoform 2 is encoded by transcript variant 2;
Williams-Beuren syndrome chromosome region 4"

>gi|22044320|ref|XM_086178.5| Homo sapiens agrin (AGRN), mRNA
Identities = 14/14 (100%)

Query: 419 ccagtggcaccgcc 432
|||||
Sbjct: 4325 ccagtggcaccgcc 4338
CDS 366..6107

>gi|4885506|ref|NM_005468.1| Homo sapiens N-acetylated alpha-linked acidic
dipeptidase-like; ILEAL DIPEPTIDYLPEPTIDASE (NAALADASEL), mRNA
Identities = 14/14 (100%)

Query: 520 cagtggcaccgccg 533
|||||
Sbjct: 1156 cagtggcaccgccg 1169
CDS 17..2239
/function="peptidase"

>gi|23943861|ref|NM_020378.1| Homo sapiens K562 cell-derived leucine-zipper-
like protein 1 (KLP1), mRNA
Identities = 15/15 (100%)

Query: 523 tggcaccgccgccg 538
|||||
Sbjct: 486 tggcaccgccgccg 500
CDS 90..710

note="K562 cells-derived leucine-zipper-like protein 1"

>gi|20384683|gb|AY030095.1| Homo sapiens pancreasin mRNA, complete cds
Identities = 17/17 (100%)

Query: 524 ggcaccgccgccgccg 540
|||||
Sbjct: 23 ggcaccgccgccgccg 7
CDS 1..873

note="CAP2; channel-activating protease 2; tryptic serine protease; similar to
marapsin"

>gi|20552317|ref|XM_096904.4| Homo sapiens Kruppel-like factor 13 (KLF13),
Identities = 15/15 (100%)

Query: 525 gcaccgccgccggcc 539
 |||||
 Sbjct: 20 gcaccgccgccggcc 34
 CDS 47..913
 note="synonyms: BTEB3, FKLF2, NSLP1, FKLF-2, RFLAT1, RFLAT-1"
 /product="similar to Krueppel-like factor 13"

>gi|14727714|ref|XM_045113.1| Homo sapiens astrotactin (ASTN), mRNA
 Identities = 15/15 (100%)

Query: 525 gcaccgccgccggcc 539
 |||||
 Sbjct: 72 gcaccgccgccggcc 58
 CDS 15..3899
 product="similar to KIAA0289"

>gi|22538424|ref|NM_145691.2| Homo sapiens ATP synthase mitochondrial F1
 complex assembly factor 2 (ATPAF2), nuclear gene encoding mitochondrial protein,
 Identities = 14/14 (100%)

Query: 525 gcaccgccgccggc 538
 |||||
 Sbjct: 947 gcaccgccgccggc 960
 CDS 154..1023

>gi|22065230|ref|XM_035037.2| Homo sapiens low density lipoprotein receptor-
 related protein 4 (LRP4), mRNA
 Identities = 14/14 (100%)

Query: 526 caccgccgccggcc 539
 |||||
 Sbjct: 2107 caccgccgccggcc 2120
 CDS 232..4839
 product="similar to MEGF7"

>gi|20545806|ref|XM_007095.6| Homo sapiens insulin receptor substrate 2
 (IRS2), mRNA
 Identities = 14/14 (100%)

Query: 526 caccgccgccggcc 539
 |||||
 Sbjct: 3613 caccgccgccggcc 3626
 CDS 516..4532

>gi|4506228|ref|NM_002809.1| Homo sapiens proteasome (prosome, macropain) 26S
 subunit, non-ATPase, 3 (PSMD3), mRNA
 Identities = 14/14 (100%)

Query: 526 caccgccgccggcc 539
 |||||
 Sbjct: 237 caccgccgccggcc 250
 CDS 158..1762

>gi|1657753|gb|U63721.1|HSU63721 Human elastin (ELN) gene, partial cds, and
 LIM-kinase (LIMK1) gene,
 Identities = 14/14 (100%)

Query: 526 caccgccgccggcc 539
 |||||
 Sbjct: 23610 caccgccgccggcc 23597

exon 23511..23730
 /gene="LIMK1"

>gi|5823551|gb|AF180522.1|AF180522 Homo sapiens intersectin short form 2
 (ITSN) mRNA, partial cds
 Identities = 14/14 (100%)

Query: 526 caccgccgccggcc 539
 |||||
 Sbjct: 158 caccgccgccggcc 171
 CDS <1..566

>gi|181652|gb|M85247.1|HUMDOPAM H.sapiens dopamine D1A receptor gene, complete
 exon 1, and exon 2, 5' end
 Identities = 14/14 (100%)

Query: 531 ccgccggccgttct 543
 |||||
 Sbjct: 1097 ccgccggccgttct 1110
 misc_signal 842..1231
 function="negative transcriptional modulator"

>gi|23395757|tpg|BK000395.1| TPA: Homo sapiens aflatoxin B1-aldehyde reductase
 (AKR7A2) mRNA,
 Identities = 14/14 (100%)

Query: 544 tcgccaccgccag 567
 |||||
 Sbjct: 312 tcgccaccgccag 299
 CDS 23..1102
 /note="aldo-keto reductase; serves as a gamma-hydroxybutyrate synthase; the
 full-length protein is predicted to contain 29 additional amino acids at the
 N-terminus that have not been recognized previously"

>gi|7706102|ref|NM_016568.1| Homo sapiens G-protein coupled receptor SALPR;
 somatostatin and angiotensin-like peptide receptor (SALPR), mRNA
 Identities = 14/14 (100%)

Query: 547 ccaccgccagaag 560
 |||||
 Sbjct: 781 ccaccgccagaag 768
 CDS 361..1770
 misc_feature 697..1527
 note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
 family)"

>gi|18568985|ref|XM_095373.1| Homo sapiens similar to Neutrophil defensin 4
 precursor (HNP-4) (HP4) (Defensin, alpha 4) (LOC157295), mRNA
 Identities = 14/14 (100%)

Query: 552 gccagaagcagcc 565
 |||||
 Sbjct: 181 gccagaagcagcc 194
 CDS 1..375
 misc_feature 145..243

>gi|22053899|ref|XM_092083.2| Homo sapiens similar to golgi autoantigen,
 golgin subfamily a, 2; golgin-95 (LOC163220), mRNA
 Identities = 14/14 (100%)

Query: 552 gccagaagcagcc 565
 |||||
 Sbjct: 505 gccagaagcagcc 518
 CDS 1..1452

>gi|22053411|ref|XM_050604.4| Homo sapiens AIE-75 binding protein protein (MCC2), mRNA
 Identities = 14/14 (100%)

Query: 553 cccagaagcagccc 566
 |||||
 Sbjct: 407 cccagaagcagccc 420
 CDS 114..2225

>gi|4505326|ref|NM_000263.1| Homo sapiens N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) (NAGLU), mRNA
 Identities = 17/18 (94%)

Query: 553 gccagaagcagcccgcc 569
 |||||
 Sbjct: 1609 gccagaagctgcccgcc 1626
 CDS 333..2564
 /function="one of four enzymes involved in the degradation of heparan sulfate; specifically removes the alpha-N-acetylglucosamine residues"

>gi|15718672|ref|NM_000683.2| Homo sapiens adrenergic, alpha-2C-, receptor (ADRA2C), mRNA
 Identities = 14/14 (100%)

Query: 553 cccagaagcagccc 566
 |||||
 Sbjct: 2530 cccagaagcagccc 2517
 CDS 892..2277
 /note="alpha2-AR-C4"
 /product="alpha-2C-adrenergic receptor"

>gi|15812179|ref|NM_004926.2| Homo sapiens zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA
 Identities = 15/15 (100%)

Query: 553 cccagaagcagcccgcg 578
 |||||
 Sbjct: 432 cccagaagcagcccgcg 446
 CDS 131..1147
 /note="EGF-response factor 1; early response factor Berg36; zinc finger protein, C3H type, 36-like 1"
 /product="butyrate response factor 1"

>gi|20556994|ref|XM_039877.5| Homo sapiens mucin 5, subtype B, tracheobronchial (MUC5B), mRNA
 Identities = 17/18 (94%)

Query: 555 cagaagcagcccgcgcc 572
 |||||
 Sbjct: 1580 cagaagcagccctccgcc 1563
 CDS 46..2688

/db_xref="MIM:600770"
 >gi|22060317|ref|XM_114498.2| Homo sapiens similar to Tcte-1 peptide (LOC202500), mRNA
 Identities = 14/14 (100%)

Query: 556 agaagcagcccgcc 569
 |||||
 Sbjct: 1317 agaagcagcccgcc 1330
 CDS 346..1401

>gi|4505032|ref|NM_000752.1| Homo sapiens leukotriene B4 receptor (LTB4R),
 Identities = 19/20 (95%)/note="Chemokine receptor-like 1"

Query: 559 agcagcccgccgcccgcga 578
 |||||
 Sbjct: 2595 agcagcccgccgcccgcga 2576 CDS: 1718..2776

>gi|1648869|emb|X98356.1|HSGPCRCO H.sapiens mRNA for G protein-coupled
 receptor
 Identities = 19/20 (95%)

Query: 559 agcagcccgccgcccgcga 578
 |||||
 Sbjct: 1266 agcagcccgccgcccgcga 1247 CDS: 389..1447

>gi|5032110|ref|NM_005634.1| Homo sapiens SRY (sex determining region Y)-box 3
 (SOX3), mRNA
 Identities = 15/15 (100%)

Query: 559 agcagcccgccgcccgcga 573
 |||||
 Sbjct: 862 agcagcccgccgcccgcga 876
 CDS 1..1332

>gi|20548635|ref|XM_167923.1| Homo sapiens homeobox protein Gsh-1 (Gsh-1),
 Identities = 14/14 (100%)

Query: 560 gcagcccgccgcccgcga 573
 |||||
 Sbjct: 116 gcagcccgccgcccgcga 129
 CDS 49..843

>gi|8923792|ref|NM_017514.1| Homo sapiens likely ortholog of mouse plexin 3
 (PLXN3), mRNA
 Identities = 14/14 (100%)

Query: 561 cagcccgccgcccgcga 574
 |||||
 Sbjct: 2896 cagcccgccgcccgcga 2909
 CDS 185..5800

>gi|9247121|gb|AF284224.1|AF284224 Homo sapiens DMRT2 and terra-like protein
 (DMRT2) bicistronic mRNA,
 Identities = 16/16 (100%)

Query: 561 cagcccgccgcccgcga 576
 |||||
 Sbjct: 111 cagcccgccgcccgcga 126
 CDS 1..681
 /note="putative transcription factor"

>gi|6179565|emb|Y19052.1|HOSA19052 Homo sapiens mRNA for doublesex-like 2
 protein (DSXL-2 gene)
 Identities = 16/16 (100%)

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Query:  561  cagcccgccgcccggcg  576
          |||||
Sbjct:  565  cagcccgccgcccggcg  580
CDS           455..1135

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Query: 561 cagcccgccgcccgg 574
      |||||
Sbjct: 213 cagcccgccgcccgg 200
      CDS 95..1840
/note="protein kinase BRPK"

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Query:  562  agcccgccgccggc 575
          |||||
Sbjct:  295  agcccgccgccggc 308
          CDS              12..1217

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Query:  564  cccgcgcgcgcgcgca  578
          |||||
Sbjct: 103  cccgcgcgcgcgcgca  89
          CDS              44..1327

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Query:564   cccgccgccggcgc 577
             |||||
Sbjct:  48   cccgccgccggcgc 35
      CDS              13..609

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Query: 576   cagcccgccgcccgc 590
           |||||
Sbjct: 2885 cagcccgccgcccgc 2899
CDS        289..3153
/note="mixed lineage kinase 2; MKN28 kinase; MKN28 derived
nonreceptor type serine/threonine kinase"
```

40

Query: 580 ttcttcccgccgcc 593
 |||||
 Sbjct: 67 ttcttcccgccgcc 80
 CDS 1..2196

>gi|13929461|ref|NM_001497.2| Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 (B4GALT1), mRNA
 Identities = 14/14 (100%)

Query: 581 tcttcccgccgccg 595
 |||||
 Sbjct: 73 tcttcccgccgccg 60
 CDS 73..1269

>gi|21359847|ref|NM_001194.2| Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 2 (HCN2), mRNA
 Identities = 14/14 (100%)

Query: 581 tcttcccgccgccg 594
 |||||
 Sbjct: 2191 tcttcccgccgccg 2204
 CDS 54..2723
 function="pacemaker channel of human heart"
 note="cyclic nucleotide-gated; brain cyclic nucleotide gated channel 2"

>gi|18032269|gb|AF274003.1|AF274003 Homo sapiens splicing-related factor RNPS1 (RNPS1) mRNA, complete cds, alternatively spliced
 Identities = 14/14 (100%)

Query:581 tcttcccgccgccg 594
 |||||
 Sbjct: 46 tcttcccgccgccg 33
 CDS 46..894

>gi|4504382|ref|NM_001528.1| Homo sapiens HGF activator (HGFAC), mRNA
 Identities = 15/15 (100%)

Query: 590 cgccgttcttctcgc 604
 |||||
 Sbjct: 1828 cgccgttcttctcgc 1814
 CDS 4..1971

>gi|14196470|ref|NM_032054.1| Homo sapiens protocadherin gamma subfamily A, 5 (PCDHGA5), transcript variant 2, mRNA
 Identities = 14/14 (100%)

Query: 600 ctgccggttcttct 613
 |||||
 Sbjct: 2416 ctgccggttcttct 2403
 CDS 1..2442

cadherin ME3"

/protein_id="NP_114443.1"

These gene clusters have an immunoglobulin-like organization, suggesting that a novel mechanism may be involved in their regulation and expression.

>gi|19923446|ref|NM_015963.2| Homo sapiens CGI-36 protein (CGI-36), mRNA
 Identities = 14/14 (100%)

Query: 600 ctgccggttcttct 613
 |||||
 Sbjct: 947 ctgccggttcttct 934

CDS 807..1565

>gi|21314399|gb|AF508782.1| Homo sapiens fibroblast growth factor 10 (FGF10)
mRNA, partial cds
Identities = 14/14 (100%)

Query: 604 ccgttcttctcaat 617
|||||
Sbjct: 173 ccgttcttctcaat 160
CDS <1..513
/function="paracrine growth factor for epithelia"
/note="keratinocyte growth factor-2; KGF2; produced by
fibroblasts of urinary bladder lamina propria"

>gi|22058975|ref|XM_172182.1| Homo sapiens similar to Ribosomal protein S5;
Minute(1)15D; Minute; transcript e (LOC255793), mRNA
Identities = 14/14 (100%)

Query: 606 gttcttctcaatgg 619
|||||
Sbjct: 405 gttcttctcaatgg 392
CDS 1..438

>gi|24797096|ref|NM_006907.2| Homo sapiens pyrroline-5-carboxylate reductase 1
(PYCR1), nuclear gene encoding mitochondrial protein, transcript variant
1, mRNA
Identities = 14/14 (100%)

Query: 607 ttcttctcaatgga 620
|||||
Sbjct: 598 ttcttctcaatgga 585
CDS 279..1238
/note="isoform 1 is encoded by transcript variant 1; P5C
reductase"

>gi|4186165|gb|L41919.1|HUMHIC1G Homo sapiens candidate tumor suppressor HIC-1
(HIC-1) gene, complete
Identities = 20/21 (95%)

Query: 626 cgccccggccgcccgcgc 646
|||||
Sbjct: 2451 cgccccggccgcccgcgcgc 2431 CDS: 637..2781
Isolation and embryonic expression of the novel mouse gene Hic1, the homologue of
HIC1, a candidate gene for the Miller-Dieker syndrome

>gi|23238250|ref|NM_032862.2| Homo sapiens tigger transposable element derived
5 (TIGD5) mRNA,
Identities = 18/19 (94%)

Query: 626 cgccccggccgcccgcgc 644
|||||
Sbjct: 510 cgccccggccgcccgcgcgc 528
CDS 1..1782

>gi|17939629|gb|BC019288.1|BC019288 Homo sapiens, hepatocyte nuclear factor 3,
beta, clone
Identities = 18/19 (94%)

Query: 626 cgccccggccgcccgcgc 644
|||||
Sbjct: 284 cgccccggccgcccgcgcgc 266

CDS <1..1370
/product="hepatocyte nuclear factor 3, beta"

>gi|22041040|ref|XM_092478.2| Homo sapiens similar to Gliacolin (LOC165257), mRNA
Identities = 21/23 (91%)

Query:628 ccccggccgcgcgcgccccacc 650
||||||| ||||||| |||||
Sbjct: 810 ccccggccgcgcgcgccccacc 788
CDS 471..1262
/product="similar to Gliacolin"

>gi|17974541|gb|AF361354.1|AF361354 Homo sapiens voltage-dependent calcium channel gamma-8 subunit(CACNG8) mRNA, complete cds
Identities = 16/16 (100%)

Query: 628 ccccggccgcgcgcgcc 643
|||||||||||||||
Sbjct: 1132 ccccggccgcgcgcgcc 1117
CDS 106..1386

>gi|24475868|ref|NM_153836.1| Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2),
Identities = 19/20 (95%)

Query: 628 ccccggccgcgcgcgccgcc 647
||||||||||||||| |||||
Sbjct: 177 ccccggccgcgcgcgcgccgcc 158
CDS 139..1011

>gi|21237772|ref|NM_016431.2| Homo sapiens mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2), transcript variant 2, mRNA
Identities = 19/19 (100%)

Query: 629 cccggccgcgcgcgccgcc 547
|||||||||||||||||
Sbjct: 1276 cccggccgcgcgcgccgcc 1294
CDS 1..2394
/note="PRKM8 interacting protein-like; JNK-interacting protein 2; islet-brain 2; JNK MAP kinase scaffold protein JIP2; homologous to mouse JIP-1"

>gi|14971412|ref|NM_015906.2| Homo sapiens tripartite motif-containing 33 (TRIM33), transcript variant alpha, mRNA
Identities = 16/16 (100%)

Query: 629 cccggccgcgcgcgcc 644
|||||||||||||||||
Sbjct: 267 cccggccgcgcgcgcc 252
CDS 85..3468

>gi|13183792|gb|AF336133.1|AF336133 Homo sapiens CECR2 protein (CECR2) mRNA, complete cds
Identities = 16/16 (100%)

Query:629 cccggccgcgcgcgcc 644
|||||||||||||||||
Sbjct: 448 cccggccgcgcgcgcc 433
CDS 419..4873

>gi|22046663|ref|XM_047536.6| Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA

Identities = 15/15 (100%)

Query:631 cggccgcgcccgcgcg 645

|||||

Sbjct: 572 cggccgcgcccgcgcg 558

CDS 45..18518

/product="similar to obscurin"

>gi|21707308|gb|BC033826.1| Homo sapiens, purinergic receptor P2X, ligand-gated ion channel, 4, clone MGC:45331 IMAGE:5216449, mRNA, complete cds

Identities = 15/15 (100%)

Query:632 ggccgcgcccgcgcgc 646

|||||

Sbjct: 24 ggccgcgcccgcgcgc 10

CDS 25..1191

/product="purinergic receptor P2X, ligand-gated ion channel, 4"

>gi|21450823|ref|NM_145056.1| Homo sapiens thymus expressed gene 3-like (MGC15476), mRNA

Identities = 16/16 (100%)

Query: 632 ggccgcgcccgcgcgc 647

|||||

Sbjct: 879 ggccgcgcccgcgcgc 894

CDS 441..1655

>gi|22652729|gb|AF489858.1| Homo sapiens serum amyloid A activating factor 2 mRNA, complete cds

Identities = 16/16 (100%)

Query:632 ggccgcgcccgcgcgc 647

|||||

Sbjct: 550 ggccgcgcccgcgcgc 565

CDS 113..1594

/note="transcription factor SAF-2"

>gi|20558544|ref|XM_028783.2| Homo sapiens opioid growth factor receptor (OGFR), mRNA

Identities = 15/15 (100%)

Query:632 ggccgcgcccgcgcgc 646

|||||

Sbjct: 174 ggccgcgcccgcgcgc 160

CDS 17..2050

/product="similar to 7-60 protein"

>gi|22042730|ref|XM_114346.2| Homo sapiens similar to source of immunodominant MHC-associated peptides (LOC201595), mRNA

Identities = 15/15 (100%)

Query:633 gccgcgcccgcgcgc 647

|||||

Sbjct: 345 gccgcgcccgcgcgc 331

CDS 200..2680

/product="similar to source of immunodominant MHC-associated peptides"

>gi|4507162|ref|NM_003107.1| Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA

Identities = 16/16 (100%)

Query:634 ccgcgccgcccgccac 649
|||||
Sbjct: 972 ccgcgccgcccgccac 957
CDS 351..1775

gi|23395757|tpg|BK000395.1| TPA: Homo sapiens aflatoxin B1-aldehyde reductase (AKR7A2) mRNA,
Identities = 18/19 (94%)

Query:640 cgcccgccaccgccgcggc 658
|||||
Sbjct: 180 cgcccgccagcgccgcggc 198
CDS 23..1102

>gi|5032110|ref|NM_005634.1| Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA
Identities = 18/18 (100%)

Query:641 gcccgccaccgccgcggc 658
|||||
Sbjct: 1044 gcccgccaccgccgcggc 1061
CDS 1..1332

>gi|20589957|ref|NM_139075.1| Homo sapiens two-pore calcium channel protein 2 (TPC2), mRNA
Identities = 15/15 (100%)

Query:643 ccgccaccgccgcgg 657
|||||
Sbjct: 160 ccgccaccgccgcgg 146
CDS 102..2360

>gi|16753218|ref|NM_033224.2| Homo sapiens purine-rich element binding protein B (PURB), mRNA
Identities = 15/15 (100%)

Query:643 ccgccaccgccgcgg 657
|||||
Sbjct: 480 ccgccaccgccgcgg 466
CDS 14..952

>gi|291945|gb|L12398.1|HUMD4C Homo sapiens dopamine receptor D4 (DRD4) mRNA, complete cds
Identities = 15/15 (100%)

Query:643 ccgccaccgccgcgg 657
|||||
Sbjct: 502 ccgccaccgccgcgg 488
CDS 1..1404

>gi|19401873|gb|AF479827.1| Homo sapiens protein kinase-like protein mRNA, complete cds
Identities = 18/19 (94%)

Query:644 cgccaccgccgcggctggg 662
|||||
Sbjct: 1907 cgccaccgccgggctggg 1889
CDS 278..2614

>gi|7542578|gb|AF241229.1|AF241229 Homo sapiens GTR-D mRNA, complete cds
Identities = 15/15 (100%)

Query: 651 gccgcggctgggccc 665
 |||||
 Sbjct: 682 gccgcggctgggccc 696 CDS: 1..768

>gi|23238193|ref|NM_148901.1| Homo sapiens tumor necrosis factor receptor superfamily, member 18 (TNFRSF18), transcript variant 2, mRNA
 Identities = 15/15 (100%)

Query: 652 gccgcggctgggccc 666
 |||||
 Sbjct: 820 gccgcggctgggccc 834 CDS: 139..906

>gi|11038623|ref|NM_004426.1| Homo sapiens polyhomeotic-like 1 (Drosophila) (PHC1), mRNA
 Identities = 15/15 (100%)

Query:671 tcttcacccttgtct 685
 |||||
 Sbjct: 1644 tcttcacccttgtct 1658
 CDS 210..3224
 /note="early development regulator 1; mouse Rae28-like"
 >gi|190395|gb|M60494.1|HUMPROFILA Human profilaggrin gene, 3' end
 Identities = 15/15 (100%)

Query:678 ccttgtcttcgtcca 692
 |||||
 Sbjct: 4236 ccttgtcttcgtcca 4222
 exon 949..4447
 CDS 1478..4447

>gi|24475953|ref|NM_013433.2| Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
 Identities = 14/14 (100%)

Query:678 ccttgtcttcgtcc 691
 |||||
 Sbjct: 2026 ccttgtcttcgtcc 2013
 CDS 292..2955
 /note="hypothetical protein FLJ12155"

>gi|8923472|ref|NM_017852.1| Homo sapiens NALP2 protein (NALP2), mRNA
 Identities = 15/15 (100%)

Query: 685 ttcgtccacgtctag 699
 |||||
 Sbjct: 453 ttcgtccacgtctag 439
 CDS 88..3276
 /note="PYRIN-Containing APAF1-like"

>gi|10198206|gb|AF298547.1| Homo sapiens nucleotide-binding site protein 1 mRNA, complete cds
 Identities = 15/15 (100%)

Query:685 ttcgtccacgtctag 699
 |||||
 Sbjct: 425 ttcgtccacgtctag 411
 CDS 78..3179
 /note="NBS1; nucleotide-binding site/leucine-rich repeat (NBS/LRR) family member"

>gi|4504576|ref|NM_002164.1| Homo sapiens indoleamine-pyrrole 2,3 dioxygenase (INDO), mRNA
Identities = 17/17 (100%)

Query:691 cacgtctagttctggga 707
|||||
Sbjct: 258 cacgtctagttctggga 274
CDS 23..1234

>Numatrin) pseudogene and the MDFI gene for MyoD family inhibitor (myogenic repressor I-MF
Identities = 15/15 (100%)

Query: 697 tagttctgggacctc 711
|||||
Sbjct: 64761 tagttctgggacctc 64775
CDS complement(64067..64810)
/note="dJ696P19.2 (NPM1 (Nucleophosmin, Numatrin) pseudogene)

>gi|22047835|ref|XM_095174.3| Homo sapiens similar to pol protein (LOC168550), mRNA
Identities = 14/14 (100%)

Query:699 gttctgggacctcc 712
|||||
Sbjct: 1249 gttctgggacctcc 1262
CDS 1..3315

>gi|4506508|ref|NM_002926.1| Homo sapiens regulator of G-protein signalling 12 (RGS12), mRNA
Identities = 15/15 (100%)

Query: 700 ttctgggacctcccg 714
|||||
Sbjct: 2786 ttctgggacctcccg 2772 CDS: 55..4185

>gi|22771013|gb|AF542391.1| Homo sapiens selectin P (granule membrane protein 140kDa, antigen CD62) (SELP) gene, complete cds
Identities = 17/18 (94%)

Query:705 ggacctcccgctcaagag 722
|||||
Sbjct: 6869 ggacctcctgctcaagag 6886
gene <1..>398

>gi|4758621|ref|NM_004770.1| Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA
Identities = 14/14 (100%)

Query:711 cccgctcaagagcc 724
|||||
Sbjct: 1329 cccgctcaagagcc 1316
CDS 3..2423

>gi|21595817|gb|BC032731.1| Homo sapiens, Wolf-Hirschhorn syndrome candidate 1, Identities = 14/14 (100%)

Query:713 cgctcaagagccag 726
|||||
Sbjct: 1876 cgctcaagagccag 1889
source 1..4239

>gi|19172410|gb|AF480461.1| Homo sapiens mixed lineage kinase-related kinase
MRK-alpha mRNA,
Identities = 14/14 (100%)

Query:715 ctcaagagccagtg 728
|||||
Sbjct: 2454 ctcaagagccagtg 2467
CDS 196..2598

>gi|23272700|gb|BC035910.1| Homo sapiens, mitogen-activated protein kinase
kinase kinase 7 interacting protein 2,
Identities = 14/14 (100%)

Query:727 tggtacaccagaag 740
|||||
Sbjct: 1758 tggtacaccagaag 1771
CDS 149..2230

>gi|10947029|ref|NM_006217.2| Homo sapiens serine (or cysteine) proteinase
inhibitor, clade I(neuroserpin), member 2 (SERPINI2), mRNA
Identities = 19/20 (95%)

Query:737 gaagtctacttttttttcta 756
|||||
Sbjct: 927 gaagtctactttttgttcta 908
CDS 34..1251

>gi|24638453|ref|NM_170665.1| Homo sapiens ATPase, Ca++ transporting, cardiac
muscle, slow twitch 2 (ATP2A2), mRNA
Identities = 14/14 (100%)

Query:765 actttgtcaccaac 778
|||||
Sbjct: 586 actttgtcaccaac 573
CDS 111..3239

>gi|21536291|ref|NM_001081.2| Homo sapiens cubilin (intrinsic factor-cobalamin
receptor) (CUBN),
Identities = 14/14 (100%)

Query:765 actttgtcaccaac 778
|||||
Sbjct: 8029 actttgtcaccaac 8042
CDS 27..10898
/note="intrinsic factor-cobalamin receptor; intrinsic factor B12-receptor"

>gi|6912355|ref|NM_012155.1| Homo sapiens echinoderm microtubule associated
protein like 2 (EML2),
Identities = 14/14 (100%)

Query:766 ctttgtcaccaact 779
|||||
Sbjct: 1595 ctttgtcaccaact 1608
CDS 36..1985

>gi|18597004|ref|XM_051693.4| Homo sapiens mitogen inducible 2 (MIG2), mRNA
Identities = 15/15 (100%)

Query: 768 ttgtcaccaacttct 782
|||||
Sbjct: 838 ttgtcaccaacttct 852

CDS: 238..2280

>gi|3335149|gb|AF055377.1|AF055377 Homo sapiens long form transcription factor C-MAF (c-maf) mRNA,
Identities = 15/15 (100%)

Query:771 tcaccaacttctcgt 785
|||||
Sbjct: 1864 tcaccaacttctcgt 1850
CDS 808..2019
/note="b-zip transcription factor"

>gi|7304920|ref|NM_013449.1| Homo sapiens bromodomain adjacent to zinc finger domain, 2A (BAZ2A),
Identities = 14/14 (100%)

Query:800 tgagtggaggacta 813
|||||
Sbjct: 1587 tgagtggaggacta 1600
CDS 740..6376

>gi|5419653|emb|AL034553.12|HS914P20 Human DNA sequence from clone RP5-914P20 on chromosome 20q13.13-13.2 Contains the gene for activity-dependent neuroprotective protein (ADNP, KIAA0784) , a PSMD10 (proteasome (prosome, macropain) 26S subunit, non-ATPase, 10) pseudogene, the DPM1 gene fo>
Identities = 19/20 (95%)

Query: 803 gtggaggactaataagactt 822
|||||
Sbjct: 10723 gtggaggactaatgagactt 10704 misc_feature: 10509..10953

>gi|14388625|gb|AF243083.1|F243081S03 Homo sapiens intrinsic factor-vitamin B12 receptor (CUBN) gene, exons 5 and 6
Identities = 16/16 (100%)

Query:817 gacttatataactgtcc 832
|||||
Sbjct: 809 gacttatataactgtcc 824
CDS AF243085.1:692..854

>gi|24527258|gb|AY071904.1| Homo sapiens ribonuclease/angiogenin inhibitor (RNH) mRNA, complete
Identities = 17/18 (94%)

Query:824 atactgtccgttctttga 841
|||||
Sbjct: 532 atactgtcagttctttga 515
CDS 1..1386

>gi|9558724|ref|NM_013291.1| Homo sapiens cleavage and polyadenylation specific factor 1, 160kDa (CPSF1), mRNA
Identities = 14/14 (100%)

Query:834 ttctttgaggaggagg 847
|||||
Sbjct: 1313 ttctttgaggaggagg 1300
CDS 52..4380

>gi|20143921|ref|NM_133437.1| Homo sapiens titin (TTN), transcript variant novex-2, mRNA
Identities = 14/14 (100%)

Query:838 ttgagggaggacct 851
 |||||
 Sbjct: 56027 ttgagggaggacct 56014
 CDS 224..81580
 /note="isoform novex-2 is encoded by transcript variant
 novex-2; connectin; CMH9, included"

Query:839 tgagggaggacctc 852
 |||||
 Sbjct: 819 tgagggaggacctc 832
 CDS 100..1155
 /product="similar to ARP2/3 complex 41 kDa subunit(P41-ARC) (Actin-related
 protein 2/3 complex subunit 1B)"

>gi|21426828|ref|NM_144773.1| Homo sapiens G protein-coupled receptor 73-like
 1 (GPR73L1), mRNA
 Identities = 14/14 (100%)

Query: 848 gacctccctatgga 861
 |||||
 Sbjct: 100 gacctccctatgga 113 CDS: 1..1155

>gi|21327026|gb|AF506288.1| Homo sapiens prokineticin receptor 2 (PKR2) mRNA,
 complete cds
 Identities = 14/14 (100%)

Query: 848 gacctccctatgga 861
 |||||
 Sbjct: 100 gacctccctatgga 113 CDS 1..1155

>gi|7669541|ref|NM_013992.1| Homo sapiens paired box gene 8 (PAX8), transcript
 variant PAX8E,
 Identities = 14/14 (100%)

Query: 849 acctccctatggac 862
 |||||
 Sbjct: 582 acctccctatggac 595 CDS 161..1024

>gi|16160856|ref|XM_007763.5| Homo sapiens myosin VA (heavy polypeptide 12,
 myoxin) (MYO5A), mRNA
 Identities = 19/20 (95%)

Query:863 cgtaactggagagtctgggg 882
 |||||
 Sbjct: 724 cgtaagtggagagtctgggg 743
 CDS 245..5812
 /product="similar to Myosin Va (Myosin 5A) (Dilute myosin
 heavy chain, non-muscle) (Myosin heavy chain 12) (Myoxin)"

>gi|4757807|ref|NM_001683.1| Homo sapiens ATPase, Ca++ transporting, plasma
 membrane 2 (ATP2B2),
 Identities = 15/15 (100%)

Query:865 taactggagagtctg 879
 |||||
 Sbjct: 1298 taactggagagtctg 1312
 CDS 577..4173
 /note="PMCA-2"

>gi|16904386|ref|NM_013363.2| Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA
Identities = 14/14 (100%)

Query: 867 actggagagtcttg 880
|||||
Sbjct: 308 actggagagtcttg 321
CDS 197..1444

>gi|7706548|ref|NM_016507.1| Homo sapiens CDC2-related protein kinase 7 (CRK7), mRNA
Identities = 15/15 (100%)

Query:868 ctggagagtctggg 882
|||||
Sbjct: 2092 ctggagagtctggg 2078
CDS 34..4506

>gi|24850118|ref|NM_170605.1| Homo sapiens PDZ domain protein (Drosophila inaD-like) (INADL), mRNA
Identities = 14/14 (100%)

Query:868 ctggagagtctggg 881
|||||
Sbjct: 1570 ctggagagtctggg 1557
CDS 1..5406

>gi|21536251|ref|NM_015678.2| Homo sapiens neurobeachin (NBEA), mRNA
Identities = 14/14 (100%)
Strand = Plus / Plus

Query:868 ctggagagtctggg 879
|||||
Sbjct: 3008 ctggagagtctggg 3021
CDS 207..9047

>gi|21434742|gb|AF467288.1| Homo sapiens BCL8B protein (BCL8B) mRNA, complete
Identities = 14/14 (100%)

Query:868 ctggagagtctggg 881
|||||
Sbjct: 3008 ctggagagtctggg 3021
CDS 207..9047

>gi|7662409|ref|NM_014963.1| Homo sapiens KIAA0963 protein (KIAA0963), mRNA
Identities = 15/15 (100%)

Query: 868 ctggagagtctggg 882
|||||
Sbjct: 2832 ctggagagtctggg 2846 CDS 216..4316

>gi|22041826|ref|XM_172259.1| Homo sapiens similar to 60S ribosomal protein L21 (LOC255888), mRNA
Identities = 16/16 (100%)

Query:869 tggagagtctggggtt 884
|||||
Sbjct: 530 tggagagtctggggtt 545
CDS 1..579

>gi|17157996|ref|NM_058167.1| Homo sapiens ubiquitin-conjugating enzyme E2, J2 (UBE2J2), mRNA
Identities = 14/14 (100%)

Query:870 ggagagtctggggt 883
 |||||
 Sbjct: 652 ggagagtctggggt 639
 CDS 205..879

>gi|23308602|ref|NM_015460.1| Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA
 Identities = 15/15 (100%)

Query:871 gagagtctgggggttc 885
 |||||
 Sbjct: 1861 gagagtctgggggttc 1847
 CDS 137..2716

>gi|6912705|ref|NM_012455.1| Homo sapiens SEC7 homolog (TIC), mRNA
 Identities = 14/14 (100%)

Query:872 agagtctgggggttc 885
 |||||
 Sbjct: 762 agagtctgggggttc 749
 CDS 64..3234
 /note="ADP-ribosylation factor guanine nucleotide-exchange factor 6"

>gi|22051239|ref|XM_048346.4| Homo sapiens insulin receptor (INSR), mRNA
 Identities = 14/14 (100%)

Query:884 tcgttgaccgtctt 897
 |||||
 Sbjct: 3251 tcgttgaccgtctt 3238
 CDS 181..4218

>gi|4507600|ref|NM_003807.1| Homo sapiens tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14), mRNA
 Identities = 14/14 (100%)

Query: 901 cggctcttacttcgg 914
 |||||
 Sbjct: 742 cggctcttacttcgg 755
 CDS 49..771

>gi|2745709|gb|U89310.1|AH005788S02 Homo sapiens nucleophosmin phosphoprotein (NPM) gene, exon 2
 Identities = 14/14 (100%)

Query: 908 acttcggttctttt 921
 |||||
 Sbjct: 411 acttcggttctttt 424 CDS U89311.1:416..535

>gi|20521002|dbj|AB002333.2| Human mRNA for KIAA0335 gene, partial cds
 Identities = 18/18 (100%)

Query: 914 gttctttttaatttcttc 931
 |||||
 Sbjct: 216 gttctttttaatttcttc 233 CDS <829..5283

>gi|19923778|ref|NM_006479.2| Homo sapiens RAD51-interacting protein (PIR51), mRNA
 Identities = 16/16 (100%)

Query:915 ttctttttaatttctt 930
|||||
Sbjct: 703 ttctttttaatttctt 688
CDS 51..1058

>gi|4505610|ref|NM_002582.1| Homo sapiens poly(A)-specific ribonuclease
(deadenylation nuclease) (PARN), mRNA
Identities = 16/16 (100%)

Query:915 ttctttttaatttctt 930
|||||
Sbjct: 1897 ttctttttaatttctt 1882
CDS 58..1977

>gi|20538519|ref|XM_057659.6| Homo sapiens similar to RIKEN cDNA 2310005N03
(LOC116228), mRNA
Identities = 18/18 (100%)

Query: 915 ttctttttaatttcttct 932
|||||
Sbjct: 629 ttctttttaatttcttct 612 CDS 337..693

>gi|18579348|ref|XM_090294.1| Homo sapiens similar to 10-
formyltetrahydrofolate dehydrogenase(LOC160428), mRNA
Identities = 19/19 (100%)

Query: 916 tctttttaatttcttctac 934
|||||
Sbjct: 2263 tctttttaatttcttctac 2245 CDS 1..2928

>gi|4503510|ref|NM_003758.1| Homo sapiens eukaryotic translation initiation
factor 3, subunit 1 alpha, 35kDa (EIF3S1), mRNA
Identities = 17/17 (100%)

Query: 916 tctttttaatttcttct 932
|||||
Sbjct: 352 tctttttaatttcttct 336 CDS 61..837

>gi|23271901|gb|BC036021.1| Homo sapiens, Similar to Bmp2-inducible kinase,
Identities = 20/21 (95%)

Query:917 cttttttaatttcttctactac 937
|||||
Sbjct: 796 cttttttaatttcttctactac 776
CDS 128..2116

>gi|18375633|ref|NM_004639.2| Homo sapiens HLA-B associated transcript 3
(BAT3), transcript variant 1, mRNA
Identities = 15/15 (100%)

Query: 931 ctactacgaggttct 945
|||||
Sbjct: 1172 ctactacgaggttct 1186 CDS 285..3683

>gi|17485359|ref|XM_066371.1| Homo sapiens LOC129184 (LOC129184), mRNA
Identities = 16/16 (100%)

Query:1016 tgtgggtgccagggtc 1031
|||||
Sbjct: 866 tgtgggtgccagggtc 851 CDS 1..960

>gi|12653994|gb|BC000795.1|BC000795 Homo sapiens, hypothetical protein.
Identities = 15/15 (100%)

Query:1017 gtgggtgccagggtc 1031
|||||
Sbjct: 306 gtgggtgccagggtc 292 CDS 49..1260

>gi|1668741|emb|X90762.1|HSHHA5GEN Homo sapiens hHa5 gene
Identities = 16/16 (100%)

Query: 1018 tgggtgccagggtctc 1033
|||||
Sbjct: 1215 tgggtgccagggtctc 1230 exon 1112..1365 number=8

>gi|18582587|ref|XM_090689.1| Homo sapiens similar to S antigen precursor -
malaria parasite(Plasmodium falciparum) (strain Wellcome) (LOC161088),
mRNA
Identities = 19/20 (95%)

Query:1019 ggggtgccagggtctcaggtg 1038
|||||
Sbjct: 372 ggggtgccagcgtctcaggtg 353 CDS 1..1221 Chr. 13

>gi|9863549|emb|AL157718.10| Human DNA sequence from clone RP11-23013 on
chromosome 20 Contains a putative novel gene, a CpG island, ESTs and GSSs,
complete sequence [Homo sapiens]
Identities = 19/20 (95%)

Query: 1021 gtgccagggtctcaggtgca 1040
|||||
Sbjct: 40364 gtgccagggtctcagctgca 40345
misc_feature complement(40329..40883) note="match: GSS: Em:AQ606491"

>gi|35258|emb|X13345.1|HSPAI19 Human gene for plasminogen activator inhibitor
1 (PAI-1) exon 9/ Identities = 19/20 (95%)

Query:1024 ccagggtctcaggtgcagac 1043
|||||
Sbjct: 264 ccagggtctcaggtggagac 245
precursor_RNA <1..1835 /note="primary transcript"

>gi|18581862|ref|XM_090590.1| Homo sapiens LOC160925 (LOC160925), mRNA
Identities = 15/15 (100%)

Query:1064 agcaactctcgagtt 1078
|||||
Sbjct: 374 agcaactctcgagtt 360 CDS 1..870

>gi|24660383|gb|BC039025.1| Homo sapiens, Similar to tyrosine 3-
monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon
polypeptide, clone MGC:47805 IMAGE:6070099, mRNA,
Identities = 17/17 (100%)

Query:1077 tttcgattttgctgtgg 1093
|||||
Sbjct: 58 tttcgattttgctgtgg 74
CDS 107..883

>gi|18253109|dbj|AB065437.1| Homo sapiens C1s gene for complement C1s,
promoter region and exon 1
Identities = 15/15 (100%)

Query: 1112 ttttcgggaaagtca 1124 (Exon wechsel)
 |||||
 Sbjct: 2584 ttttcgggaaagtca 2570
 promoter 1..2826
 /function="complement activation"
 exon 2827..2978

>gi|22047240|ref|XM_175003.1| Homo sapiens LOC256626 (LOC256626), mRNA
 Identities = 15/15 (100%)

Query: 1785 gaaaagtgacctgaa 1799
 |||||
 Sbjct: 1768 gaaaagtgacctgaa 1754 CDS 1..1914

>gi|11990557|gb|AF170052.1|AF170052 HIV-2 isolate 97227 from France envelope
 glycoprotein (env) gene, partial cds
 Identities = 15/15 (100%)

Query: 1825 gtatggcctctgtcc 1839
 |||||
 Sbjct: 866 gtatggcctctgtcc 852 CDS <1..>2243

>gi|4502528|ref|NM_000721.1| Homo sapiens calcium channel, voltage-dependent,
 alpha 1E subunit(CACNA1E), mRNA, note="brain specific"
 Identities = 15/15 (100%)

Query: 1827 atggcctctgtccgg 1841
 |||||
 Sbjct: 1433 atggcctctgtccgg 1419 CDS 166..6921

>gi|20559017|ref|XM_166786.1| Homo sapiens similar to SUMO-1 activating enzyme
 subunit 1; SUMO-1 activating enzyme E1 N subunit; sentrin/SUMO-activating
 protein AOS1; ubiquitin-like protein SUMO-1 activating enzyme (LOC220311), mRNA
 Identities = 16/16 (100%)

Query: 1842 gatacacacggggaag 1857
 |||||
 Sbjct: 886 gatacacacggggaag 901 CDS 1..1134

/gene="LOC220311">gi|4758617|ref|NM_004693.1| Homo sapiens cytokeratin type II
 (K6HF), mRNA
 Identities = 16/16 (100%)

Query: 1845 acacacggggaagctg 1860
 |||||
 Sbjct: 366 acacacggggaagctg 351 CDS 19..1674

>gi|17149843|ref|NM_057092.1| Homo sapiens FK506 binding protein 2, 13kDa
 (FKBP2), transcript variant 2, mRNA
 Identities = 14/14 (100%)

Query:1847 acacggggaagctg 1860
 |||||
 Sbjct: 269 acacggggaagctg 282
 CDS 103..531
 misc_feature 223..504
 /note="FKBP; Region: FKBP-type peptidyl-prolyl cis-trans isomerase"

>gi|20127426|ref|NM_002252.2| Homo sapiens potassium voltage-gated channel,
 delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA

Identities = 15/15 (100%)

Query:1847 acacggggaagctgc 1861
|||||
Sbjct: 653 acacggggaagctgc 667
CDS 403..1878

>gi|24981010|gb|BC039695.1| Homo sapiens, Janus kinase 2 (a protein tyrosine kinase), clone
Identities = 14/14 (100%)

Query:1865 cattattcttcaaa 1878
|||||
Sbjct: 3354 cattattcttcaaa 3341
CDS 108..3497

>gi|20149552|ref|NM_004414.3| Homo sapiens Down syndrome critical region gene 1 (DSCR1), mRNA
Identities = 15/15 (100%)

Query:1872 cttcaaacgagtcag 1886
|||||
Sbjct: 215 cttcaaacgagtcag 229
CDS 66..659

>gi|6648540|gb|U53821.1|HSU53821 Homo sapiens adapt78 protein gene, partial
Identities = 15/15 (100%)

Query:1872 cttcaaacgagtcag 1886
|||||
Sbjct: 219 cttcaaacgagtcag 233
CDS 70..>562

>gi|8922685|ref|NM_018228.1| Homo sapiens hypothetical protein FLJ10811 (FLJ10811), mRNA
Identities = 17/17 (100%)

Query: 1955 ctggaagagctggggcc 1971
|||||
Sbjct: 923 ctggaagagctggggcc 907 CDS 146..2254

>gi|17298301|gb|AF283402.1|F283327S74 Homo sapiens candidate tumor suppressor protein (LRP1B) gene, exon 76
Identities = 17/17 (100%)

Query: 2034 ttcttaaaatttttact 2050
|||||
Sbjct: 307 ttcttaaaatttttact 291 CDS
join(AF283376.1:<285..407,AF283377

>gi|20545629|ref|XM_121159.1| Homo sapiens LOC206321 (LOC206321), mRNA
Identities = 25/28 (89%)

Query: 2133 agatagaacgagacattagagcaaagtt 2161
||||| |
Sbjct: 527 agatagaacgagatctgagagcaaagtt 500 CDS 1..1176

>gi|22054646|ref|XM_069110.2| Homo sapiens similar to hypothetical protein FLJ23231 (LOC134973), mRNA
Identities = 16/16 (100%)

Query: 2155 caaagtttttgttcca 2170

|||||

Sbjct: 915 caaagtttttgttcca 930 CDS 1..2475

>gi|6382057|ref|NM_007313.1| Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1(ABL1), transcript variant b, mRNA

Identities = 18/18 (100%)

Query: 2163 ttgttccacaaaaacatt 2180

|||||

Sbjct: 135 ttgttccacaaaaacatt 118 CDS 1..3447

>gi|3095103|gb|AF044579.1|AF044579 Homo sapiens translocation related non-coding gene (TNRG10) mRNA, complete sequence

Identities = 17/17 (100%)

Query: 2164 tgttccacaaaaacatt 2180

|||||

Sbjct: 2361 tgttccacaaaaacatt 2345

gene 1..2726

repeat_region 326..547

repeat_region 2599..2709

Intron (BB/SHR)

>gi|5453963|ref|NM_006251.1| Homo sapiens protein kinase, AMP-activated, alpha 1 catalytic subunit (PRKAA1), mRNA

Identities = 16/16 (100%)

Query: 316 tcttctgagcactcaa 331

|||||

Sbjct: 943 tcttctgagcactcaa 928

CDS 24..1676

note="AMPK alpha 1; Protein kinase, AMP-activated, catalytic, alpha-1"

>gi|23503326|ref|NM_018682.2| Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) (MLL5), mRNA

Identities = 16/16 (100%)

Query: 365 catcagatgaaggatc 380

|||||

Sbjct: 1003 catcagatgaaggatc 988

CDS 202..5778

/note="contains PHD and SET domains; similar to Drosophila trithorax"

/product="myeloid/lymphoid or mixed-lineage leukemia 5

>gi|1418773|emb|X97186.1|HSE14 H.sapiens mRNA for E14 protein

Identities = 17/17 (100%)

Query: 428 gaagacaaagagttctt 444

|||||

Sbjct: 1509 gaagacaaagagttctt 1493

CDS 35..4318

>gi|1381666|gb|U58852.1|HSU58852 Human NPAT mRNA, complete cds

Identities = 17/17 (100%)

Query: 428 gaagacaaagagttctt 444

|||||

Sbjct: 1475 gaagacaaagagttctt 1459

CDS 1..3528

/note="predicted amino acids have three regions which share similarity to annotated domains of transcriptional factor oct-1, nucleolus-cytoplasm shuttle phosphoprotein and protein kinases"

>gi|22065878|ref|XM_040846.5| Homo sapiens nuclear protein, ataxia-telangiectasia locus (NPAT),
Identities = 17/17 (100%)

Query: 428 gaagacaaagagttctt 444
|||||
Sbjct: 1509 gaagacaaagagttctt 1493
CDS 35..4318
/product="similar to NPAT"

>gi|18079322|ref|NM_080612.1| Homo sapiens GRB2-associated binding protein 3 (GAB3), mRNA
Identities = 17/17 (100%)

Query: 578 ggggtccaagaccagag 594
|||||
Sbjct: 1254 ggggtccaagaccagag 1238
CDS 33..1793
/function="differentiation signaling"

>gi|20270211|ref|NM_033396.1| Homo sapiens tankyrase 1 binding protein 1, 182kDa (TNKS1BP1), mRNA
Identities = 16/16 (100%)

Query: 583 ccaagaccagagtaaa 598
|||||
Sbjct: 2725 ccaagaccagagtaaa 2740
CDS 308..5497
/product="tankyrase 1-binding protein of 182 kDa"

>gi|21626462|ref|NM_000038.2| Homo sapiens adenomatosis polyposis coli (APC),
Identities = 16/16 (100%)

Query: 616 gacaaaaaggaactg 631
|||||
Sbjct: 8232 gacaaaaaggaactg 8247
CDS 39..8570
/product="adenomatosis polyposis coli"